



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 163765

**TO: Phuong Bui**  
**Art Unit: 1638**  
**Location: REM 2C18/2A15**  
**Serial Number: 107734698**

**Wednesday, August 31, 2005**

**From: Beverly Shears**  
**Location: Biotech-Chem Library**  
**REM 1A54**  
**Phone: 571-272-2528**  
**beverly.shears@uspto.gov**

### Search Notes

#### Protein Sequence Searches – February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (uniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.



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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 30, 2005, 18:36:04 ; Search time 5037.58 Seconds  
(without alignments)  
11220.746 Million cell updates/sec

Title: US-10-734-698A-38  
Perfect score: 1485  
Sequence: 1 AGCCAAAGCCCCACTCAACCA.....CAAAAGAAATGTCGAAGTT 1485

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues  
Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*

- 1: gb\_est1:\*
- 2: gb\_est2:\*
- 3: gb\_hic:\*
- 4: gb\_est3:\*
- 5: gb\_est4:\*
- 6: gb\_est5:\*
- 7: gb\_est6:\*
- 8: gb\_gss1:\*
- 9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	819.6	55.2	1191	9	CL970400 OaIFCC041
2	813.4	54.8	1191	9	CL958884 OaIFCC036
3	748	50.4	772	6	CA800424 eaui15h12.
4	744.6	50.1	1912	3	AY109333 Zea mays
5	736.8	49.6	740	7	CK606439 gmrhRw6-
6	729	49.1	775	4	BI968543 GM830005B
7	716.6	48.3	760	2	BE660984 469 GmaxS
8	706.8	47.6	969	7	CK276743 EST722821
9	701.8	47.3	967	7	CK230599 EST753313
10	698.4	47.0	1400	3	CNSDA7B6 Arabidops
11	695.4	46.8	954	7	CK263461 EST709539
12	690.4	46.5	1498	3	CNSDA7V6 Arabidops
13	685	46.1	1235	6	CB330707 SPST664
14	673.6	45.4	1008	7	CK269428 EST715506
15	669.6	45.1	979	7	CK274045 EST720123
16	667	44.9	946	7	CK263343 EST709421
17	658.8	44.4	670	7	CF806716 psHB015XD
18	658.8	44.4	933	7	CK270799 EST716877
19	654	44.0	965	7	CK277099 EST723177
20	652.4	43.9	879	6	CB893745 EST646537
21	651.2	43.9	872	7	CK250566 EST734203
22	649	43.7	1011	7	CK162737 FGAS01533
23	648.8	43.7	732	6	CA798979 sat73d06.
24	645.6	43.5	954	7	CK269124 EST715202

25	645	43.4	922	6	CB981331	CB981331 CAB70004 -
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27	641.8	43.2	902	7	CK279131	CK279131 EST752509
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30	639	43.0	926	7	CF355380	CF355380 V-B-127E0
31	638	43.0	866	7	CO115240	CO115240 GR_E5016
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33	636	42.8	918	7	CK272097	CK272097 EST718175
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35	631	42.5	958	5	BQ165469	BQ165469 EST611338
36	627.8	42.3	959	7	CK361083	CK361083 EST707161
37	626.2	42.2	637	4	BI942096	BI942096 sf16a09.x
38	636	42.2	937	7	CK277371	CK277371 EST723449
39	625.8	42.1	632	6	CA851546	CA851546 D14H08 P0
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44	625.2	42.1	942	7	CK277159	CK277159 EST723237
45	623.2	42.0	793	7	CF921046	CF921046 gmrhRw3 -

## ALIGNMENTS

RESULT 1  
LOCUS CL970400 1191 bp DNA linear GSS 21-SEP-2004  
DEFINITION OaIFCC041243 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.  
ACCESSION CL970400  
VERSION CL970400.1 GI:52395409  
KEYWORDS GSS.  
SOURCE Oryza sativa (indica cultivar-group)  
ORGANISM Oryza sativa (indica cultivar-group)  
REFERENCE 1 (bases 1 to 1191)  
AUTHORS Ma, L., Wang, C., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M., Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L., Wong, G. K. S., Deng, X. W. and Wang, J.  
TITLE An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis  
JOURNAL Unpublished (2004)  
COMMENT Contact: Chen Chen  
Department of Bioinformatic  
Beijing Institute of Genomics  
Chinese Academy of Sciences, Beijing 101300, China  
Tel: 86-10-80481559  
Fax: 86-10-80488676  
Email: chenchen@genomics.org.cn  
Rice genomic sequence.  
Class: exon-trapped.  
Location/Qualifiers  
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/clone\_lib="Oryza sativa Express Library"  
/note="Oryza sativa exon trapped genomic sequences"

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Best Local Similarity 81.0%; Pred. No. 5.3e-220;  
Matches 954; Conservative 0; Mismatches 224; Indels 0; Gaps 0;  
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DB 13 GATACCTTCCTCTTACCTCGAGTCTGTGAACAGAGGACCCCTGACAGCTCTGCGAC 72  
QY 140 CAAATCTCCGATGCTGTCTCTCGACGCTTGCCTTGAACAGGACCCACGACAGCAAGGTTGCC 199

Db	73	CAAGTCTCAGATGCTGTGCTTGAATGCTGCTGGCCGAGGACCCTGACACCAAGGTCGCT	132
Qy	200	TGCGAACAATGCACCAAGACCAACTTGGTCATGGTCTTCGGAGAGATCACCCACCAAGGCC	259
Db	133	TGTGAGACCTGCGACCAAGACCAACATGGTCATGGTCTTTGGTGAGATCACCAACAGGCT	192
Qy	260	AACGTTGACTACGAGAAAGATCGTGCGTGACACCTGCAGGAACATCGGCTTCGTCTCAAAAC	319
Db	193	AACGTGACCTATGAGAAGATTGTGAGGAGACATGCCGTAAACATCGGTTTGTGTGACGT	252
Qy	320	GATGTGGGACTTGATGCTGCAAACTGCAAGGTCTTTGTAAACATTTAGCAGCAGAGGCCCT	379
Db	253	GATGTCGGTCTCGATGCTGACCACTGCAAGGTGCTTGTGAACATCGAGCAGCAGTCCCT	312
Qy	380	GATATTGCCCGGGTGTGACGGCCACCTTACCAAAAGACCCGAGGAATCGGTGCTGGA	439
Db	313	GACATTTGCAAGGGTGTGCAACGGCCACTTACCAGCGCCCTGAGGAGATTGTTGCTGGT	372
Qy	440	GACCAGGCTCACATGTTTGGCTATGCCCACCGACGAAACCCAGAAATTTGATGCCATTTGAGT	499
Db	373	GACCAGGACACATGTTTGGATATGCAACTGTATGAGACCCCTGAGTTGATGCCCTTCAGC	432
Qy	500	CATGTTCTTGCAACTAAACTCGGTGCTGCTCACCGAGTTTGCAGAAACGGAACCTGTC	559
Db	433	CATGCTCTTGCTACCAAGCTTGGCGTCTGTTACGGAAAGTTCCGAAGAATGGGACCTGC	492
Qy	560	CCATGTTGAGGCTGATGGGAAAACCCAAAGTGACTTTGAGTATTTACATGACACAGGT	619
Db	493	GCATGSGCTGAGGCTGACGGGAAGACCCAAAGTGACTGTTGAGTACCCGAATGAGAGCGGT	552
Qy	620	GCCATGTTCCAGTTCTGTGTCACACATGTGCTTATCTCCACCCAAATGATGAGACTGTG	679
Db	553	GCCAGGCTCCTGTCCGTGTTCCACACCGTCTCATCTTACCNGCATGATGAGACAGTC	612
Qy	680	ACCAACGACGAAATTTGACGTGACCTCAAGGAGCATGTGATCAAGCCGGTGATCCCGGAG	739
Db	613	ACCAACGATGAGATTGCTGCTGACCTGAAGGAGCATGTCTCAAGCCGTCTCATCCCGAG	672
Qy	740	AAGTACCTTGTAGAAAGACCAATTTTCCATTTGNAACCCCTCTGGCCGTTTGTTCATTTGA	799
Db	673	CAGTACCTTTGATGAAAGACCAATCTTCCATCTTAAACCCATCTGGTTCGCTTCGTCATTTGC	732
Qy	800	GGTCCTCACGGTGATGCTGCTCTCACGGCGCGAAGATCATCTCGATATCTTACGAGGA	859
Db	733	GGACCTCATGGTGATGCTGCTCAGTGGCCGAGAGATCATCTTGACCTTATGGTGGC	792
Qy	860	TGGGGTGCTCATGGTGGTGGTCTTCTCCGGGAAGGATCCCAACAGGTTGATAGGAGT	919
Db	793	TGGGGAGCTCAGCGTGGTGGTGGCTTCTCTGGCAAGGACCCCAACCAAGGTTGACCCGAGT	852
Qy	920	GGTGCTTACATTTGAGACAGGCTGCTTAAGACATTTGTGCGAAGTGAATAGCCAGAGG	979
Db	853	GGAGCATACGTGCGAAGCGAAGCTGCCAAGAGCAATTTGCTAGTGGCCCTTGTGCGCGCT	912
Qy	980	TGCATTGTGCAAGTGTCTTATGCAATGGTGTGCGCGAGCTTTGTCTGTCTTTGTTGAC	1039
Db	913	TGCATTGTCCAAGTATCATACGCCATCGTGTGCCAGAGCCACTGTCCGTTATTCGTCCAC	972
Qy	1040	ACCTATGGCACCGGGAAGATCCATGATTAAGGAGATTCTCAACATTTGTAAGGAGAACTTT	1099
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Qy	1100	GATTTACGGCCCGGTATGATCTCATCAACTTGATCTCAAGAGGGGTGGGAATAACAGG	1159
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Qy	1160	TTCTTTGAAGACTGCTGCATATGGACATTCGGCAGAGAGGACCTGACTTACATGGGAA	1219
Db	1093	TACCTCAAGACGGCGGCTTACGGTCACTTTCGGAAGGACGACCCAGACTTCACTCTGGAG	1152
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Db	1153	GTGTGAAGCCCTCAAGTGGGAGAACCTTCTGCCTA	1190
RESULT 2			
CL958884			
LOCUS	CL958884		
DEFINITION	OaIFC036463 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.		
ACCESSION	CL958884		
VERSION	CL958884.1	GI:52372525	
KEYWORDS	GAS.		
SOURCE	Oryza sativa (indica cultivar-group)		
ORGANISM	Oryza sativa (indica cultivar-group) Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.		
REFERENCE	1 (bases 1 to 1191)		
AUTHORS	Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M., Zhao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L., Wong, G.K.S., Deng, X.W. and Wang, J.		
TITLE	An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis		
JOURNAL	Unpublished (2004)		
COMMENT	Contact: Chen Chen Department of Bioinformatic Beijing Institute of Genomics Chinese Academy of Sciences, Beijing 101300, China Tel: 86-10-80481559 Fax: 86-10-80488676 Email: chenchen@genomics.org.cn Rice genomic sequence. Class: exon-trapped.		
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ORIGIN			
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Best Local Similarity	80.8%;	Pred. No. 3e-218;	
Matches	949;	Conservative 0;	Mismatches 226; Indels 0; Gaps 0;
Qy	76	GGCAGACATTCCTATTACCTCAGAGTCAGTGAACGAGGACACCTGCACAGCTCTG 135	
Db	9	GGTTGACACCTTCTCTTCACTTCGAGTCGTCGATGAGGACACCTGCACAGCTCTG 68	
Qy	136	CGACCAATCTCCGATCTGCTTCGACGCTTGCTTGAACAGGACCCAGACAGCAAGGT 195	
Db	69	CGACCATATCCGATGGGTGCTTGATGCTGCTTGAAGACCTGAAAGCAAGGT 128	
Qy	196	TGCTCGGAACATGCAACGACCACTTGGTTCATGCTTCGAGAGATCACACCAA 255	
Db	129	TGCTGTGAGACCTGCACCAAGACCAATGCTCATGCTGTTGGTGAGATCACTACCA 188	
Qy	256	GGCCAACTTGACTACGAGAGATCGTCGTCGACCTGCAGGAAACATCGCTTCGTC 315	
Db	189	GGCCAAATGTGACTATGAGAAGATCGTCAGGATACCTTGCCTGGGATCGCTTTGTC 248	
Qy	316	AAACGATGTGGACTTGATGCTGCAACTGCAAGGTCTTGTAAACATTTGACGACGAG 375	
Db	249	CNATGATGTAGGCCCTTGATGCTGAACACTGTAAAGTCTTGTCAACATTTGACGACCA 308	
Qy	376	CCCTGATTTGCCAGGGTGTGACGGCCACTTTACAAAGACCCGAGGAATCGGTGC 435	
Db	309	CCCTGACATCGACAGGGTGTCCATGGCACTTCAACAAAGCCGACGAGGATTTGGTGC 368	
Qy	436	TGGAGACCGGGTCAATGTTGGCTATGCCAGGAGAACCCAGATTTGATGCCATT 495	
Db	369	CGGTGACAGGGGCATATGTTGGATATGCAACCGATGAGACCCCTGAATTTGATGCCACT 428	





QY 448 TCACATGTTGGCTATGCCAGGACGAACCCAGAAATGATGCCATTGAGTCATGTTCT 507  
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 Db 421 TCACATGTTGGCTATGCCAGGACGAGACCCAGAAATGATGCCATTGAGTCATGTTCT 480  
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 QY 568 GAGGCTGATGGGAAACCAAGTGA CTGTTGAGTATTAACAATGACAACGGTGCCATGGT 627  
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## RESULT 4

AY109333/c  
 LOCUS AY109333 1912 bp mRNA linear HTC 17-OCT-2002  
 DEFINITION Zea mays CL2757\_5 mRNA sequence.

ACCESSION AY109333

VERSION AY109333.1

KEYWORDS GI:21212903

SOURCE HTC.

ORGANISM Zea mays

Ze mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD Clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 1912)  
 Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whiteitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.

Maize Mapping Project/DuPont Consensus Sequences for Design of

Overgo Probes

Unpublished (2002)

2 (bases 1 to 1912)

Coe,E.H.

Direct Submission

Submitted (25-APR-2002) Maize Mapping Project, University of

Missouri, Columbia, MO 65211, USA

If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, [maizemap.org](http://maizemap.org); ZmDB, [www.zmdb.iastate.edu](http://www.zmdb.iastate.edu); TIGR, [www.tigr.org](http://www.tigr.org); or NCBI, [www.ncbi.nlm.nih.gov](http://www.ncbi.nlm.nih.gov). When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: [www.zmdb.iastate.edu](http://www.zmdb.iastate.edu).

## FEATURES

source

1. 1912  
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 /db\_xref="taxon:4577"  
 /clone\_lib="Maize Mapping Project/DuPont Consensus Library"

/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

## ORIGIN

Query Match 50.1%; Score 744.6; DB 3; Length 1912;  
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Best Local Similarity 76.2%; Pred. No. 1e-198;  
 Matches 926; Conservative 0; Mismatches 280; Indels 9; Gaps 2;  
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Db 585 GACTTCAGGCCCCGGGATGATCAGCATCAACCTCGACCTGAAGAAGGGCGG---CAACAGG 529  
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 QY 1220 GTGGTCAAGCCCTCAAGTGGGAGAGGCGCTAAGGCCATTCAATCCACTGCAATGTGCTG 1279  
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 QY 1280 GGAGTTTTTTAGCGT 1294  
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RESULT 5  
 CK506439 740 bp mRNA linear EST 22-JAN-2004  
 LOCUS gmhrw6-12\_D09\_T7 Soybean root hair subtracted cDNA library  
 DEFINITION gmhrw6 Glycine max cDNA, mRNA sequence.

ACCESSION CK506439  
 VERSION CK506439.1 GI:41146228  
 KEYWORDS EST.

SOURCE Glycine max (soybean)  
 ORGANISM Glycine max  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
 Glycine.

REFERENCE 1 (bases 1 to 740)  
 AUTHORS Scheffler, B.E., Huang, S., Liu, X., Nguyen, H., Duke, M. and Stacey, G.  
 TITLE Expressed sequence tags from soybean root hair subtractive cDNA  
 JOURNAL library  
 COMMENT Unpublished (2003)

Contact: Gary Stacey  
 University of Missouri  
 108 Waters Hall, Columbia, MO 65211, USA  
 Tel: 573-884-4752  
 Fax: 573-882-0588  
 Email: staceyg@missouri.edu  
 Single pass sequence  
 Seq primer: T7.

FEATURES  
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 /mol\_type="mRNA"  
 /cultivar="Williams 82"  
 /db\_xref="taxon:3847"  
 /tissue\_type="root hairs"  
 /clone\_lib="Soybean root hair subtracted cDNA library  
 gmhrw6"  
 /note="Organ: root hairs; Vector: pCEM-T-Easy; cDNA clones  
 generated from soybean root hair tissue treated with  
 Bradyrhizobium japonicum for 6 hours."

ORIGIN  
 Query Match 49.6%; Score 736.8; DB 7; Length 740;  
 Best Local Similarity 99.7%; Pred. No. 1.2e-196;  
 Matches 738; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 746 CTTGATGAGAAGACCAATTTTCCACTTGAACCCCTCTGGCCGTTTGTGTCATTGGAGTGCT 805  
 Db 1 CTTGATGAGAAGACCAATTTTCCACTTGAACCCCTCTGGCCGTTTGTGTCATTGGAGTGCT 60  
 QY 806 CACGGTGATGCTGCTCTACCGGCCCAAGATCATCATGACTTACGGAGATGGGT 865  
 Db 61 CACGGTGATGCTGCTCTACCGGCCCAAGATCATCATGACTTACGGAGATGGGT 120  
 QY 866 GCTCATGGTGGTGGTCTTTCTCCGGGAAGGATCCCAAGGTTGATAGGAGTGCTGT 925  
 Db 121 GCTCATGGTGGTGGTGGTCTTTCTCCGGGAAGGATCCCAAGGTTGATAGGAGTGCTGT 180  
 QY 926 TACATTGTGAGACAGCGCTGCTAAGAGCATTTGTGGCAAGTGGACTAGCCAGAAGGTGCATT 985

Db 181 TACATTGTGAGACAGCGCTGCTAAGAGCATTTGTGGCAAGTGGACTAGCCAGAAGGTGCATT 240  
 QY 986 GTGCAAGTGTCTTATGTCATTCGATTCGCGAGCCCTTTGTCTGTCTTTGTCACACCTAT 1045  
 Db 241 GTGCAAGTGTCTTATGTCATTCGATTCGCGAGCCCTTTGTCTGTCTTTGTCACACCTAT 300  
 QY 1046 GGCACCGGGAAGATCCATGATTAAGAGATTTCTCAACATTGTGAAGGAGAATTTGATTTTC 1105  
 Db 301 GGCACCGGGAAGATCCATGATTAAGAGATTTCTCAACATTGTGAAGGAGAATTTGATTTTC 360  
 QY 1106 AGGCCCGGTATGATCTCCATCAACCTTGATCTCAAGAGGGGTGGGAATACAGGTTCTTG 1165  
 Db 361 AGGCCCGGTATGATCTCCATCAACCTTGATCTCAAGAGGGGTGGGAATACAGGTTCTTG 420  
 QY 1166 AAGACTGTGTCATATGGACACTTCGCGAGAGAGGCCCTGACTTCACATGGGAAGTGGTC 1225  
 Db 421 AAGACTGTGTCATATGGACACTTCGCGAGAGAGGCCCTGACTTCACATGGGAAGTGGTC 480  
 QY 1226 AAGCCCCCTCAAGTGGGAGAAGGCCCTAAGGCCATTCAATCCACTGCAATGTGCTGGAGTT 1285  
 Db 481 AAGCCCCCTCAAGTGGGAGAAGGCCCTAAGGCCATTCAATCCACTGCAATGTGCTGGAGTT 540  
 QY 1286 TTTTAGCGTTGCGCTTATAATGCTCTATTATCCATTAACCTTCCACGTCCTCTGCTGTGT 1345  
 Db 541 TTTTAGCGTTGCTCTTATAATGCTCTATTATCCATAAATTTCCACGTCCTCTGCTGTGT 600  
 QY 1346 TTTTCTCTCGTCGCTCCTCTCTATTTTGTCTCTCTGCTCTTCTGCTCTTAAATTTTAC 1405  
 Db 601 TTTTCTCTCGTCGCTCCTCTCTATTTTGTCTCTGCTCTTCTGCTCTTAAATTTTAC 660  
 QY 1406 ATGATCAACTAAAAAATGACTCTCTGTTTCCGACCAATGCTCTCTTAAATATCAGTAT 1465  
 Db 661 ATGATCAACTAAAAAATGACTCTCTGTTTCCGACCAATGCTCTCTTAAATATCAGTAT 720  
 QY 1466 CAAAAAAGATGTTCCAAGTT 1485  
 Db 721 CAAAAAAGATGTTCCAAGTT 740

RESULT 6  
 BI968543/c 775 bp mRNA linear EST 23-OCT-2001  
 LOCUS GM830005BI2E10 Gm-r1083 Glycine max cDNA clone Gm-r1083-1771 3',  
 DEFINITION mRNA sequence.

ACCESSION BI968543  
 VERSION BI968543.1 GI:16342948  
 KEYWORDS EST.

SOURCE Glycine max (soybean)  
 ORGANISM Glycine max  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
 Glycine.

REFERENCE 1 (bases 1 to 775)  
 AUTHORS Vodkin, L., Keim, P., Shoemaker, R., Retzel, E., Khanna, A., Corvett, V.,  
 Expelling, J., Raph, C., Shoop, E., Pardinas, J., Liu, L. and Lewin, H.  
 TITLE A Functional Genomics Program for Soybean (NSF 9872565)  
 JOURNAL Unpublished (1999)  
 COMMENT Other ESTs: AW132830 corresponding to Gm-cl013-3165 (5')  
 Contact: Vodkin, L.O., PI, A Functional Genomics Program for  
 Soybean (NSF 9872565)  
 Lewin, H. A., Director, Keck Center for Comparative and Functional  
 Genomics

University of Illinois  
 Edwin R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA  
 Tel: (217) 244-6147  
 Fax: (217) 333-4582  
 Email: l-vodkin@uiuc.edu  
 This clone is available through: Incyte Genomics, 4633 World  
 Parkway Circle St. Louis, Missouri 63134. Phone (800) 430-0030 or  
 (314) 427-3222 FAX: (314) 427-3324. Web site:  
 http://www.incyte.com/reagents/catalog.jsp?page=clones/collaboratio





```
Db 364 GAAGTCGCGAAGATGGCACCTGCCCTGCTGTTGAGCGCTGATGGCAAACTCAAGTTACT 423
QY 596 GTTGAGTATTACAATGACAAACGGTGCATGGTTCCAGTTTCGTTGTCGATCGTGTATTC 655
Db 424 GTTGAGTATTGCAATGACAAATGGTGCATGATTTCCAAATTAAGGTACACACTGTTCTTATC 483
QY 656 TCCACCCACATGATGAGTCTGACCAACGAGGAATTCGACGTGACCTCAAGGAGCAT 715
Db 484 TCCACCCACATGAGACCGTTACAAATGATGAGATTGCCCGGAGCCTTAAGGAGCAT 543
QY 716 GTGATCAACCGGTGATCCCGAGAGTACCTTTGATGAGAGACACATTTTCCACTTGAAC 775
Db 544 GTATCAACCGAGTCATCCAGAGAGTACCTTTGACGAGAGACATCTTCCACCTTAAC 603
QY 776 CCTCTGGCGGTTTGTCTATTTGAGAGTCTTCACGGTGATGCTGGTCTCACCGCGCGAAG 835
Db 604 CCATCTGGCGGATTTGTTATTGGTGACCTCATGTGTGATGCTGGTCTCATCTGGTGTAAA 663
QY 836 ATCATCATGATCTTACCGAGGATGGGTGCTCATGTGTGGTGTCTTCTCCGGGAG 895
Db 664 ATCATCATGATGACATATGTTGGGTGCTCATGTGTGGTGTCTTCTCCGGGAG 723
QY 896 GATCCCAACCAAGTTGATAGGAGTGTGCTTACATTTGACAGACAGGCTGCTAAGGAGCAT 955
Db 724 GACCCCAACCAAGTTGACAGGAGTGTGATACATCGTTAAGCAAGCTGCAAGAGTATT 783
QY 956 GTGGCAAGTGGACTACCGAAGAGTGCATTTGCAAGTGTCTTATGCCATGCGTGTGCCC 1015
Db 784 GTAGCTAGTGGACTGCTCGCAGATGCATCGTGCAGGTTTCTTATGCCATCGTGTGCT 843
QY 1016 GAGCCTTGTCTGCTTGTTCACACCTATGACCGGGAAGATCCATGATAGGAGATT 1075
Db 844 GAGCCTTGTCTGATTTGTGACACCTATGGACCTGGAAGATCCCGCAAGGAAATT 903
QY 1076 CTCAACATTTGTGAAGAGAACTTTGATTTTCAGCGCCGGTATGATCTCCATCAACCTTGAT 1135
Db 904 TTGAGATCGTTAAGGAGAACTTCGACTTCAGACCTGGAAATGATGTCCATAAATTTGGAT 963
QY 1136 CTCAAG 1141
Db 964 TTGAAG 969
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## RESULT 9

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CK290599
LOCUS
DEFINITION
  CK290599 967 bp mRNA linear EST 02-AUG-2004
  EST75313 Nicotiana benthamiana mixed tissue cDNA library,
  normalized, full-length Nicotiana benthamiana cDNA clone NEMBW02 5',
  end, mRNA sequence.
```

```
ACCESSION
VERSION
KEYWORDS
SOURCE
  CK290599.1 GI:39870224
  EST.
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## ORGANISM

```
Nicotiana benthamiana
  Nicotiana benthamiana
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  asterids; lamids; Solanales; Solanaceae; Nicotiana.
```

## REFERENCE

```
AUTHORS
  Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
  Staskawicz, B., Jin, H. and Baker, B.
  Generation of EST sequences from Nicotiana benthamiana
  Unpublished (2003)
```

## TITLE

Contact: Robin Buell

## JOURNAL

The Institute for Genomic Research

## COMMENT

9712 Medical Center Dr, Rockville, MD 20850, USA  
Email: potato-array@tigr.org  
Clones can be requested from the University of Arizona Genomics  
Institute via <http://genome.arizona.edu/orders/>.

## Seq primer:

ATT TAG GTG ACA CTA TAG.

## Location/Qualifiers

1..967

/organism="Nicotiana benthamiana"

/mol\_type="mRNA"

## FEATURES

source

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/db_xref="taxon:4100"
/clone="NEMBW02"
/tissue_type="abiotic and biotic stress-treated leaves,
callus tissue and root tissue"
/lab_host="DH10B-Tona"
/clone_lib="Nicotiana benthamiana mixed tissue cDNA
library, normalized, full-length"
/notes="Vector: pCMVSPORT6.1; Site_1: EcoRI; Site_2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (Pseudomonas syringae pv tomato 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."
```

## ORIGIN

```
Query Match 47.3%; Score 701.8; DB 7; Length 967;
Best Local Similarity 83.5%; Pred. No. 1e-186;
Matches 796; Conservative 0; Mismatches 157; Indels 0; Gaps 0;

QY 80 GAGCATTTCTTATTACCTCAGAGTCAGTGAACGAGGACACCTGACAAGCTCTGCCAC 139
Db 15 GAAATTTTCTTATTACCTCCGAGTCTGTGAACGAGGTCACCCAGACAAGCTCTGTGAT 74
QY 140 CAAATCTCCGATGCTGCTCCGACGCTTGCCTTGAACAGAGCCACGACAGCAAGGTTGCC 199
Db 75 CAGATCTCTGATGAGTTCTTGTATGCTGCTTGTAGCAAGATCTCTGAGCAAGGTTGCC 134
QY 200 TGCAGAAATGCAACCAAGACCAACTTGTGTATGCTCTTCGGAGAGATCACCAAGGCC 259
Db 135 TGTGAAATCTTCAGCAAGACCAACTTGTGTATGCTCTTGTGTGATCACCAAGGCT 194
QY 260 AACGTTGACTACGAGAAGATCGTGTGACACCTGACAGAAACATCGGCTTCGTCTCAAC 319
Db 195 AATGTAGACTATGAGAAGATTGTGGCGACACATGCCGTAATTTGGATTTGTTCCGAT 254
QY 320 GATGTGGACTTGATGTGACAACTGCAAGGTCCTTGTAAACATTTGACAGCAGAGCCCT 379
Db 255 GATGTTGGCTTGTATGCTGACAACTGCAAGGTCCTTGTATACATTTGACAGCAAAAGTCT 314
QY 380 GATATGCCCAGGTTGTGCACGGCCACTTACAAAAGACCCGAGGAAATCGTGCTGCA 439
Db 315 GATATCGCTCAAGGTGTCCACGGCCATCTGACCAAAACGCTGAGGAGATTGGTCTGGT 374
QY 440 GACCAGGTCACATGTTTGGGTATGCCACGACGAAACCCAGAAATTCATGCCATTGAGT 499
Db 375 GACCAGGACACATGTTTCGGGTATGCCACAGATGAGACCCCTGATTTGATGCTCTCAGC 434
QY 500 CATGTTCTTGCAACTAAACTCGTGCTGCTCTCACCGAGGTTTCGCAAGAACGGAACCTGC 559
Db 435 CATGTTCTGCAACTAAACTTTGGTGGCCGCTCTCACTGAAGTCCGCAAGATGTTACCTGC 494
QY 560 CCATGTTGAGGCTGATGGGAAACCCCAAGTACTGTTGAGTATTACATGACACAGCGT 619
Db 495 CCCTGGTTGAGGCGCGATGGCAAGACCCCAAGTTACTGTTGAGTACTACATGACAAATGT 554
QY 620 GCCATGTTTCAGTTTCGTTGCCACACTGCTTATCTCCACCAACATGATGAGACTGTG 679
Db 555 GCCATGTTTCAGTTTAGGTTCCACTGTTCTCATCTCCACTCAACAGATGAGACTGTT 614
QY 680 ACCAACGACGAAATTTGACAGTGAACCTCAAGGACATGTGATCAAGCCGGTATCCCGAG 739
Db 615 ACTAATGATGAGATTGCCCGGAGACCTTAAGGAACATGTGTCATCAAGCCAGTCTATCCAG 674
QY 740 AAGTACCTTGTGAGAGACCATTTTCCACTTGAACCCCTCTGGCCGTTTGTCTATTGGA 799
Db 675 AAGTACCTTGTGAGAGACCAATCTTCCACCTTAACCCATCTGCGCCGATTCGTTATGGT 734
QY 800 GGTCTCTACCGGTGATGCTGGTCTCACCGGCGCAAGATCATCATCTTACGAGGA 859
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QY 1186 CTTTGGCAGAGAGGCCCTGACTTCACATGGGAAGTGGTCAAGCCCTCAAGTGGAGAA 1245  
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 Db 1149 CTTTGAAGGACGATGCTGATTTTACCTGGGAGGTAGTCAAGTACTCAAGTCTAAACA 1208  
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 QY 1246 GGCCTAAG 1253  
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 Db 1209 GGTCCAAG 1216

RESULT 11  
 CK263461 954 bp mRNA linear EST 03-AUG-2004  
 DEFINITION EST709539 potato abiotic stress cDNA library Solanum tuberosum cDNA  
 clone FOABM65 5' end, mRNA sequence.

ACCESSION CK263461  
 VERSION CK263461.1 GI:39820439  
 KEYWORDS EST.  
 SOURCE Solanum tuberosum (potato)

ORGANISM Solanum tuberosum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 asterids; lamiales; Solanales; Solanaceae; Solanum.

REFERENCE Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.

1 (bases 1 to 954)  
 Generation of ESTs from abiotic stressed potato tissue

Other ESTs: EST709540

CONTACT: Robin Buell

The Institute for Genomic Research

9712 Medical Center Dr, Rockville, MD 20850, USA

Email: potato-array@igr.org

Clones can be requested from the University of Arizona Genomics

Institute via http://genome.arizona.edu/orders/

Seq primer: ATT TAG GTG ACA CTA TAG.

Location/Qualifiers

1..954

/organism="Solanum tuberosum"

/mol\_type="mRNA"

/cultivar="Kennebec"

/db\_xref="taxon:4113"

/clone="FOABM65"

/tissue\_type="abiotic stress treated leaf and root tissue"

/lab\_host="PH10B-TonA"

/clone\_lib="potato abiotic stress cDNA library"

/note="Vector: pCMVSPORT6.1; Site1: EcoRI; Site2: NotI;

supplier: Solanum tuberosum var. Kennebec plants were

grown from cuttings on a 16hr light/8 hr dark cycle at 25

C for 3-4 weeks. Abiotic stress conditions were applied to

four separate sets of plants. Set 1 involved saturation of

the soil with 150 mM NaCl and tissues were harvested at

following application of the salt stress (leaves: 2hr,

6hr, 12hr, 1d, 2d, and 4d; roots: 2hr, 6hr, 12hr, and 2d).

Set 2 were grown under the standard conditions and then

were water stressed by withdrawal of further watering

applications. Drought stressed plants were harvested after

cessation of watering (leaves: 3d, 5d, and 7d; roots: 3d

and 5d). Set 3 were grown under the standard conditions

and then were cold stressed by placement at 4 C. Cold

stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,

and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,

and 4d were grown under the standard conditions and

then were heat stressed by placement at 35 C. Heat

stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,

2d and 4d and heat-stressed roots were harvested at 6 hr,

12 hr, 1 d, and 4d. RNA was isolated from all tissues and

equal RNA from each tissue and stress was pooled to

construct the cDNA library. RNA sample."

# ORIGIN

Query Match 46.8%; Score 695.4; DB 7; Length 954;  
 Best Local Similarity 83.1%; Pred. NO. 6.7e-185;  
 Matches 792; Conservative 0; Mismatches 161; Indels 0; Gaps 0;

QY 194 GTTCTGCTCGAAAACATGCAACAGACCAACTTGGTTCATGGTCTTCGAGAGAGATCACACC 253  
 |||||  
 Db 1 GTTGCAATGTGAAACTTGCACCAAGACCAACTTGGTTCATGGTCTTCGAGAGATCACAGC 60  
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 QY 254 AAGCCCAACGTTGACTACGAGAAAGATCGTGGTCAACCTCGACCTCGAGAAACATCGGCTTCGTC 313  
 |||||  
 Db 61 AAGCTATTGTAGACTATGAGAAGATTGTGGCTGACACATCGCGTAATATTGGATTGTT 120  
 |||||  
 QY 314 TCAACAGATGGGACCTTGATCTGACAACTGCAAGGTCTTGTAAACATTTAGCAGCAG 373  
 |||||  
 Db 121 TCTGATGATGTGGTCTTGGTCTGATAAATGCAAGGTCTTGTATTATTTAGAGAGCAA 180  
 |||||  
 QY 374 AGCCTGATATTGCCAGGGTGTGCACGGCCACCTTACCAAAAGACCCGAGAAATCGGT 433  
 |||||  
 Db 181 AGTCTGATATTGTCAAGGTGTCCACGGCCATTTGACCAAAACGCCCCGAGAGATTGGT 240  
 |||||  
 QY 434 GCTGGAGACCAAGGTTCAATGTTTGGTATGCCACGAGCAAAACCCCAAGAAATTTGATGCA 493  
 |||||  
 Db 241 GCTGGTACCAAGGTTCAATGTTTGGCTATGCCACGATGAGACCCCTGAATTTAATGCT 300  
 |||||  
 QY 494 TTGATCATGTTTGGCAACTAAACTCGGTCTCTCACGGAGTTTCGCAAGAACGGA 553  
 |||||  
 Db 301 CTCAGTCACTGCTTGGCAACTAAACTTGGTCCCGCTTTACAGAAAGTCCGCAAGAAATGGC 360  
 |||||  
 QY 554 ACCTGCCCATGTTGAGGCTGTGAGGAAAACCCCAAGTGAAGTGTGAGTATTACAATGAC 613  
 |||||  
 Db 361 ACCTGCCCTGTTGAGGCTGTGAGGAAAACCCCAAGTGAAGTGTGAGTATTACAATGAC 420  
 |||||  
 QY 614 AACGGTCCATGTTTCCAGTTCGTTCCACTGTCACACTGTCGTTATCTCCACCAACATGATGAG 673  
 |||||  
 Db 421 AATGGTGCATGATTTCCAAATTAAGGTACACACTGTTCTTATCTCCACCAACACGATGAG 480  
 |||||  
 QY 674 ACTGTGACCAACGAGAAATTTGCACTGACCTCAAGGAGCATGTGATCAAGCCGGTGATC 733  
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 Db 481 ACCGTTACAAATGATGAGATTGCCCGGACCTTAAGGAGCATGTGATCAAGCCAGTCAATC 540  
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 QY 734 CCGGAGAAAGTACCTTTGATGAGAAGACCAATTTTCCACTTTGAACCCCTCTGGCCGTTTGTGC 793  
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 Db 541 CCAGAGAATGATCTTGGAGAGAGACCAATCTTCCACCTTTAACCCTCTGGCCGATTGTT 600  
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 QY 794 ATTGAGAGTCTCTACGGTGTGATGCTGTCTACCGGCCCAAGATCATCATGATCTTAC 853  
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 Db 601 ATTGGTGACCTCATGTTGATGCTGCTCACTGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 660  
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 QY 854 GGAGGATGGGTGCTCATGTTGTTGTTCTTCCGGGAGAGATCCCAACCAAGGTTGAT 913  
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 Db 661 GGTGTTGGGGTGTCTCATGTTGTTGTTCTTCTCGGGCAAGGACCCCAACCAAGGTTGAT 720  
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 QY 914 AGGAGTGTGCTTACATTTGTGAGACAGGCTGTCTAAGAGCATTTGTGGCAAGTGGACTAGCC 973  
 |||||  
 Db 721 AGGAGTGTGATACATCTGTAAGGCAAGCTGCNAAGAGTATTGTAGCTAGTGGACTCGCT 780  
 |||||  
 QY 974 AGAAGGTGCATTTGTCAAAGTGTCTTATGCCATTTGGTGTGCCGAGCCCTTTGTCTCTTT 1033  
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 Db 781 GCGAGATGCATCGTGCAGGTTTCTTATGCCATCGGTGTGCTGTGAGCCATTTGTCTGTATT 840  
 |||||  
 QY 1034 GTTGACCATATGGCAGCGGAGATCCATGATAGGAGATTTCTCAACATTTGTGAAGGAG 1093  
 |||||  
 Db 841 GTTGACATCTATGGCAGTGGAAAGATCCCGCAAGGAAATTTTGAAGATCTGTTAAGGAG 900  
 |||||  
 QY 1094 AACTTTGATTTTCAGGCCCGGTATGATCTCCATCTCAACCTTTGATCTCAAGAGGGG 1146  
 |||||  
 Db 901 AACTTCGATTTTCAGACCTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 953  
 |||||

RESULT 12

LOCUS CNS0A7V6

DEFINITION Arabidopsis thaliana Full-length cDNA Complete sequence from clone

GSUTLS602H07 of Adult vegetative tissue of strain col-0 of

Arabidopsis thaliana (thale cress).

ACCESSION BX823645

VERSION BX823645.1 GI:42466477

CNS0A7V6 1498 bp mRNA linear HTC 06-FEB-2004

Arabidopsis thaliana Full-length cDNA Complete sequence from clone

GSUTLS602H07 of Adult vegetative tissue of strain col-0 of

Arabidopsis thaliana (thale cress).

ACCESSION BX823645

VERSION BX823645.1 GI:42466477



KEYWORDS HTC; GSLT cDNA.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana

REFERENCE 1 (bases 1 to 1498)  
AUTHORS Castell, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J., and Salanoubat, M.  
TITLE Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation

JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1498)  
AUTHORS Genoscope.  
TITLE Direct Submission  
JOURNAL Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 131 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

COMMENT The sequences are based on single pass reads.  
Life Technologies (a division of Invitrogen) members carried out full-length libraries construction : Temple G.  
Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.  
URGV INRA : Clepet C., Caboche M.  
Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.  
http://www.genoscope.cns.fr/externe/sequences/Banque\_Projet\_BF/Full length  
http://www.genoscope.cns.fr/cgi-bin/ggb?source=Arabidopsis.

FEATURES  
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/clone="GSLTSL602H07"  
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/plasmid="PCWSPORT 6"  
/gene="At3g17390"

ORIGIN  
Query Match 46.5%; Score 690.4; DB 3; Length 1498;  
Best Local Similarity 75.9%; Pred. No. 2e-183;  
Matches 892; Conservative 0; Mismatches 281; Indels 3; Gaps 3;

QY 80 GAGACATTCCTATTTACCTCAGAGTCAGTGAACGAGGACACCCCTGACAAAGCTCTCGGAC 139  
DB 72 GAATCTTTTGTTCACATCTGATCCGTCAAGGAGGACATCCCGAAGCTTTGTGAT 131

QY 140 CAAATCTCCGATGCTGCTCGACGCTTGCTTGAACAGGACCCGACAGCAAGGTGCTC 199  
DB 132 CAGATCTCCGACGCTATCTCGATGCTGCTTGAACAGACCCCTGAGAGCAAGGTGCT 191

QY 200 TGGGAACATGACCAAGACCAACTTGGTCATGCTTCGGAGAGATCAACCAAGGCC 259  
DB 192 TGTGACACTTGTACCAAGACTAAACATGGTTCATGGTTTGGAGAAATCAACCAAGGCT 251

QY 260 AAGTTGACTACGAGAGATCGTGGCTGACCTGACGAGCAACATCGGCTTCGCTCTCAAC 319  
DB 252 AAGTTGATACGAGCAGATTGTTCTGTAACATGCGGTGAGATTGGATTGCTCTGCT 311

QY 320 GATGTGGGACTTGATGCTGCAACTGCAAGGCTCTTGTAAACATTGAGCAGCAGCCCT 379  
DB 312 GAGCTTGGTCTAGATCTGACAAATTCGAGGTTCTGTTAAACATTGAGCAACAGAGTCT 371

QY 380 GATATTTGCCAGGCTGTGACGGCCACCTTACCAAAAGACCCGAGGAAATCGGTGTGGA 439  
DB 372 GACATTGCAAGGTTTCATGGTCTATCTCACTAAGAGCCGAGAGGTTGGAGCTGCT 431

QY 440 GACCAAGGTCACATGTTTGGCTATGCGACGAGCAAAACCCAGAAATTGATGCCATTGAGT 499  
DB 432 GACCAAGGTCACATGTTTGGGTATGCTACTGATGAGACTCCTGAGCTCATGCTCTTACT 491

QY 500 CATGTTCTTGCAACTAACTCGTGTCTCTCACGAGGTTGCGAAGAACGAACTGCTGC 559  
DB 492 CAGGTTCTCGCTACTAAGCTTGGAGCTAACTCACTGAAGTTTGGCAAGAAATGGAACCTG 551

QY 560 CATGTTCTGAGGCTGATGGGAAACCCAAAGTACTGTTGAGTATTACAAATGACAAAGCT 619  
DB 552 CTTGTTGAGGCCAGATGTTAAGCTCAAGTCACTATTGAGTATCATCAACGAAACGGGA 611

QY 620 GCATGTTTCCAGTTCTGTTCCACACTGTGCTTATCTCCACCCAAACATGATGAGACTGTG 679  
DB 612 GCATGTTTCTGTAGTCTGTCACACTGTTCTCATCTCAACACAGCATGACGAGACTGTG 671

QY 680 ACCAAGCAGAAATTCAGCTGACCTCAAGGAGCATGTGATCAAGCCGCTGATCCCGGAG 739  
DB 672 ACTAAGCATCATCCACCTCATCTTCCACCAACATCTCATCAACCCAGTATCCAGAC 731

QY 740 AAGTACCTTGATGAGAAGACCAATTTTCCACTTTGMAACCCCTCTGGCCGTTTGTGTCATTGGA 799  
DB 732 AATACCTTGATGAGAAGAACCAATCTTCCATCTCAACCCATCTGGTCTGTTTGTATCCGA 791

QY 800 GGTCTCTACGCTGATGCTGCTCTCACGGCCGCAAGATCATCATCGATACTTACGAGGA 859  
DB 792 CGTCTCATTTTATTTCTTTCTTACTGCGTAAATCAAGATGATATTTATTTT 851

QY 860 TGGGTGCTCATGTTGGTGGTCTTTCTCGGGAAGGATCCCAACCAAGGTTGATGAGAGT 919  
DB 852 TGTTTTTCACA-CTTATTTGTGCTTCTCTGTAATGACCCAAACCAAGGTTGACATTAT 910

QY 920 GGTGCTTACATGTCAGACAGGCTCTAAGACATTTGTGGCAAGTGGATAGCCAGGAAG 979  
DB 911 GGGGCTTACATCTTTTATTCAGACGCTAATATCATTTAGCAGCTTGGCTAGCGAGCGG 970

QY 980 TGCATTGTGCAAGTCTCTTATGCCATTGGTGTGCCCGAGCCCTTTGTCTGCTTTGT-TGA 1038  
DB 971 GTCAATTTGTTCAAGTCTCGTATGCCATTTTTCCTCGAGCCATTGTCGTGTTTGTGTCGA 1030

QY 1039 CACCTATGCGACCGGGAAGATCCATGATGAAGAGATTCTCAACATTTGGAAGGAGAACTT 1098  
DB 1031 CAGTTATGGAACAGGAAAGATACCAAGACAAAGGAGATTCTTGAGATTGTGAGGAGAGTT 1090

QY 1099 TGATT-TCAGGCCCGGTATGATCTCCATCAACCTTGATCTCAAGAGGGTGGGAATAACA 1157  
DB 1091 TGATTCTCAGGCCAGGTATGATCTCCATTAACCTTGATCTGAAGAGAGGAGGTAATGGTA 1150

QY 1158 GGTTCCTGAAAGACTCTCATATGACACACTTCGGCAGAGAGGACCCCTGACTTTCATGCGG 1217  
DB 1151 GGTTCCTGAAAGACTCTGCTGCTATGTCATTTGGGAAGGAGCGATGCTGATTTCACTGGG 1210

QY 1218 AAGTGGTCAAGCCCTCAAGTGGGAGAAGCGCTAAG 1253  
DB 1211 AGGTAGTCAAGCCACTCAAGTCTAACAAGGTTCCAAG 1246

RESULT 13  
CB330707  
LOCUS  
DEFINITION  
SpEST664 Sweetpotato cDNA library Ipomoea batatas cDNA 5', 3'  
similar to S-adenosyl-L-methionine synthetase mRNA, mRNA sequence.

ACCESSION  
CB330707  
VERSION  
CB330707.1  
GI:28879836  
EST.  
SOURCE  
Ipomoea batatas (sweet potato)  
ORGANISM  
Ipomoea batatas  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; lamids; Solanales; Convolvulaceae; Ipomoeaceae; Ipomoea.  
REFERENCE  
1 (bases 1 to 1235)  
AUTHORS  
Jankowicz, J., Berenyi, M. and Burg, K.

TITLE Identification of adaptation specific differences in the mRNA  
expression profile of drought tolerant and sensitive sweetpotato  
Unpublished (2004)  
JOURNAL  
COMMENT Contact: Berenyi M.  
Department of Biotechnology  
ARC Seibersdorf Research GesmbH  
A2444 Seibersdorf, Austria  
Tel: +43 50550 3524  
Fax: +43 50550 3444  
Email: Maria.Berenyi@arcs.ac.at  
PCR Primers  
FORWARD: lambda Triplex 5' Screening Amplimer  
BACKWARD: lambda Triplex 3' Screening Amplimer  
Insert Length: 1235 Std Error: 0.00  
Seq primer: lambda Triplex Sequencing Primers  
POLYA=Yes.

## FEATURES

source

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/organism="Ipomoea batatas"  
/mol\_type="mRNA"  
/db\_xref="taxon:4120"  
/tissue\_type="Leaf"  
/lab\_host="Lambda"  
/clone\_lib="Sweetpotato cDNA library"  
/note="Vector: Triplex2; Site 1: Sfi A; Site 2: Sfi B;  
Ipomoea batata (Lam) L.; Smart cDNA library Construction  
Kit; Clontech: PT3000-1"

ORIGIN  
Query Match 46.1%; Score 685; DB 6; Length 1235;  
Best Local Similarity 83.4%; Pred. No. 6.4e-182;  
Matches 778; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

QY 321 ATGTGGACTTGATGCTGCAACTGCAAGTCTTGTAACATTTGAGCAGAGCCCTG 380  
Db 1 ATGTTGGTTGGATGCTGCAACTGCAAGTCTTGTAACATTTGAGCAGAGCTCTG 60

QY 381 ATATTGCCAGGGTGTGACGGCCACTTACCAAGAGCCCGAGAAATCGTGTGGAG 440  
Db 61 ATATTGCCAGGGTGTGACGGCCACTTACCAAGAGAGCTGAGATATTTGTTGGTG 120

QY 441 ACCAGGTCACATGTTTGGCTATGCCACGAGCAAAACCCAGAAATTTGATGCCATTGAGTC 500  
Db 121 ACCAGGGCCACATGTTGGATATGTCACGACGAGACCCTGAAATTTGATGCCCTCAGCC 180

QY 501 ATGTTCTTCCAACTAACTCGGTCTGCTCTCACCAGGTTTCGCAAGAACGGAACTCGCC 560  
Db 181 ATGTCCTTGCACCAAGCTTGGAGCTCGCCTCACCAGGTCGGAAGGATGGGACCTGG 240

QY 561 CATGTTGAGGCTGATGGGAAACCCCAAGTCACTGTTGAGTATTACATGACACAGGTTG 620  
Db 241 CTTGGCTCAGACTGATGTTGAAACTCAGGTCACTGTTGAGTACTACATGACATGGTG 300

QY 621 CCATGTTCCAGTTCGTTGCCACACTGCTCTTATCTCCACCCAAACATGATGAGACTGTGA 680  
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Db 361 CCAATGATGAATTCGCTCGTGATCTCAAGGACGATGTCAATCAAGCTGTGATTCGCGAGA 420

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QY 801 GTCCTCAGCGTGATGCTGCTCACCGGCGGCAAGATCATCATCATCTTACCGGAGGAT 860  
Db 481 GACCTCATGTTGATGCTGGGCTCACTGGCGGCAAGATCATTTATGACATACGTTGAT 540

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Db 541 GGGGTGCTCAGGAGGAGTGCTTTCTCAGGGAAGACCCCTACCAAGGTGGACAGAGTG 600

QY 921 GTGCTTCAATTTGAGACAGGCTGCTAAGACGATTTGGCAAGTGGACTAGCAGAGGT 980  
Db 601 GAGCTATGCTGTGAGGCAAGCTGCCAAGACATTTGTCACACGGGCTTCTCGTAGGT 660

QY 981 GCATTTGTGCAAGTGTCTTATGCCATTTGGTGTCCGAGCCCTTTGTCTCTTTGTGTGACA 1040  
Db 661 GCATTTGTGAGGTGTCTATCGCCATTTGGTGTGCTGCAACCATTTGTCCCTCTTCGTAGATA 720

QY 1041 CCTATGGCACCGGAAGATCCATGATAGGAGATTTCTCAACATTTGTGAGGAGACTTTG 1100  
Db 721 CCTATGGAAACCGGAAGATTTCCGCAAGGAATTCCTCAAGATTTGTGAAGAGACATTTG 780

QY 1101 ATTTTCAGCCCGGTATGATCTCCATCAACTTGTATCTCAAGAGGGGTGGGATACAGGT 1160  
Db 781 ATTTTCAGCCCTGATGATGATCGCCATCAACTTGGACCTCAAGAGGGGTGGCAACAGCAGGT 840

QY 1161 TCTTGAAGACTGTCTCATATGAGACATTTCCGACAGAGGACCTGACTTCATCTGAGGAAG 1220  
Db 841 TCTTGAAGACCGCTCTTATGGCCATTTCCGATAGGATGACCTGACTTCATCTGAGGAAG 900

QY 1221 TGGTCAAGCCCTCAAGTGGGAGAGGCTTAAG 1253  
Db 901 TGGTGAAGCCCTCTCAAGTGGGACAAACCTCAAG 933

## RESULT 14

CK269428

LOCUS

DEFINITION

CK269428

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

## FEATURES

source

1..1008  
/organism="Solanum tuberosum"  
/mol\_type="mRNA"  
/cultivar="Kennebec"  
/db\_xref="taxon:4113"  
/clone="POACM76"  
/tissue\_type="abiotic stress treated leaf and root tissue"  
/lab\_host="DH10B-TonA"  
/clone\_lib="potato abiotic stress cDNA library"  
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;  
supplier: Solanum tuberosum var. Kennebec plants were  
grown from cuttings on a 16hr light/8 hr dark cycle at 25  
C for 3-4 weeks. Abiotic stress conditions were applied to  
four separate sets of plants. Set 1 involved saturation of  
the soil with 150 mM NaCl and tissues were harvested at  
following application of the salt stress (leaves: 2hr,  
6hr, 12hr, 1d, 2d, and 4d; roots: 2hr, 6hr, 12hr, and 2d).  
Set 2 were grown under the standard conditions and then  
were water stressed by withdrawal of further watering  
applications. Drought stressed plants were harvested after  
cessation of watering (leaves: 3d, 5d, and 7d; roots: 3d  
and 5d). Set 3 were grown under the standard conditions

and then were cold stressed by placement at 4 C. Cold stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d. Set 4 were grown under the standard conditions and then were heat stressed by placement at 35 C. Heat stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d and 4d and heat-stressed roots were harvested at 6 hr, 12 hr, 1 d, and 4d. RNA was isolated from all tissues and equal RNA from each tissue and stress was pooled to construct the cDNA library. RNA sample."

ORIGIN

Query Match 45.4%; Score 673.6; DB 7; Length 1008;  
Best Local Similarity 83.8%; Pred. No. 1e-178;  
Matches 774; Conservative 0; Mismatches 149; Indels 1; Gaps 1;

QY 80 GAGACATTCCTATTACCTCAGAGTCAGTGAACGAGGAGCACCTCGACAGCTCTCGAC 139  
DB 86 GAAACTTCTATTACCTCTGAGTCTGTAACGAGGTCACCCAGACAGCTCTGTGAT 145  
QY 140 CAAATCTCCGATCTGTCTCGACGCTTGCTTGAACAGGACCCAGACAGCAAGGTTGCC 199  
DB 146 CAGATCTCTGATCGAGTCTTGTGATGCTGCTTGAGCAAGATCTCGAGCAAGTTGCA 205  
QY 200 TCGGAACATGCAACCAAGACCAACTTGGTCATGCTTTCGAGAGATCAACCAAGGCC 259  
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QY 260 AAGCTTGACTACGAGAGATCGTGGTGACCTGCAGGACATCGGCTTCGCTCAAC 319  
DB 266 ATTGTAGATCATGAGAAGATCGTGGTGAGACATCGCGTAATATTGGATTGTTCTGAT 325  
QY 320 GATGTGGGACTTGATGCTGCAAACTGCAAGGTCCTTGTAAACATTGAGCAGCAGAGCCCT 379  
DB 326 GATGTTGGTCTTGATGCTGACAACTGCAAGTCTTGTACATTGAGCAGCAAGTCTCT 385  
QY 380 GATATTGCCAGGGTGTGACGGCCACTTTACAAAGACCCGAGGAATTCGGTGTGGA 439  
DB 386 GATATTGCTCAAGGTGTCAATGGCCACTGTACCAACCGCCGAGGAGATTTGGTGTGT 445  
QY 440 GACCAGGTCACATGTTTGGCTATGCCAGGACGAAACCCAGAAATGTGATGCTTGGT 499  
DB 446 GACCAGGTCACATGTTTGGCTATGCCAGGACGAAACCCAGAAATGTGATGCTTGGT 505  
QY 500 CATGTTCTTGCAACTAACTCGGTGCTCGTCTCACCGAGTTCGCAAGAACGGAACCTGC 559  
DB 506 CAGTCTCTTGCACTAACTTGTGTCGCTTACCGAAGTCGCAAGATGTGACTCTGC 565  
QY 560 CCATGTTGAGGCTGATGGGAAAAACCAAGTGACTGTTGAGTATTACATGACAAAGGT 619  
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QY 620 GCATGTTTCCAGTTCGTGTCACATGTCCTTATCTCCACCAACATGATGAGCTGTG 679  
DB 626 GCATGATTTCCATCAGGGTCCACATGTGCTTATCTCCACTCAACATGATGAGCCGT 685  
QY 680 ACCAAGCAGAAATTCGAGCTGACCTCAAGGAGCATGTGATCAAGCCGCTGATCCCGAG 739  
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QY 740 AAGTACTTGTGAGAAGACCAATTTTCCACTTGAACCCCTCTGGCGTTTGTTCATTTGA 799  
DB 746 AAGTACTTGTGAGAAGACCAATTTTCCACTTGAACCCCTCTGGCGTTTGTTCATTTGT 805  
QY 800 GGTCTCTCAGGTGATCTGCTCACCAGGCGCAAGATCATCATCATCTTACGAGAGA 859  
DB 806 GGAACCTCATGGTGTCTGCTCTCACTGGTCTGTAAT-ATCATCATCGACACTTATGGTGT 864  
QY 860 TGGGGTGTCTCATGGTGTGTGCTTTCTCGGGAAGGATCCCAACCAAGGTTGATAGGCT 919  
DB 865 TGGGGTGTCTCATGGTGTGTGCTTTCTCTGGCCAGGACCCCAACCAAGGTTGACAGGT 924  
QY 920 GGTGCTTTACATTTGTGAGACAGGCTGCTAAAGACATTTGTGGCAAGTGGACTAGCCAGAGG 979

Db 925 GTGTCATACATCCTTAGGCGAGGCTGCAAGAGCTATTGTAGCTAGTGCCTCGCAGA 984  
QY 980 TGCATTGTCAAAGTGTCTTATGCC 1003  
Db 985 TGCATGCTGACAGTTTCTTATGCC 1008

RESULT 15

CK274045 979 bp mRNA linear EST 03-AUG-2004  
EST720123 potato abiotic stress cDNA library Solanum tuberosum cDNA  
clone POAD891 5' end, mRNA sequence.  
CK274045  
CK274045.1 GI:39831023  
EST.  
Solanum tuberosum (potato)  
Solanum tuberosum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; lamids; Solanales; Solanaceae; Solanum.  
1 (bases 1 to 979)  
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.  
Generation of ESTs from abiotic stressed potato tissue  
Unpublished (2003)  
Other ESTs: EST720124  
Contact: Robin Buell  
The Institute for Genomic Research  
9712 Medical Center Dr, Rockville, MD 20850, USA  
Email: potato-array@igr.org  
Clones can be requested from the University of Arizona Genomics  
Institute via http://genome.arizona.edu/orders/  
Seq primer: AAT TAG GTG ACA CTA TAG.

FEATURES

Location/Qualifiers  
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/organism="Solanum tuberosum"  
/mol\_type="mRNA"  
/cultivar="Kennebec"  
/db\_xref="taxon:4113"  
/clone="POAD891"  
/tissue\_type="abiotic stress treated leaf and root tissue"  
/lab\_host="DH10B-Tona"  
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;  
supplier: Solanum tuberosum var. Kennebec plants were  
grown from cuttings on a 16hr light/8 hr dark cycle at 25  
C for 3-4 weeks. Abiotic stress conditions were applied to  
four separate sets of plants. Set 1 involved saturation of  
the soil with 150 mM NaCl and tissues were harvested at  
following application of the salt stress (leaves: 2hr,  
6hr, 12hr, 1d, 2d, and 4d; roots: 2hr, 6hr, 12hr, and 2d).  
Set 2 were grown under the standard conditions and then  
were water stressed by withdrawal of further watering  
applications. Drought stressed plants were harvested after  
cessation of watering (leaves: 3d, 5d, and 7d; roots: 3d  
and 5d). Set 3 were grown under the standard conditions  
and then were cold stressed by placement at 4 C. Cold  
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,  
and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,  
2d. Set 4 were grown under the standard conditions and  
then were heat stressed by placement at 35 C. Heat  
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,  
2d and 4d and heat-stressed roots were harvested at 6 hr,  
12 hr, 1 d, and 4d. RNA was isolated from all tissues and  
equal RNA from each tissue and stress was pooled to  
construct the cDNA library. RNA sample."

ORIGIN

Query Match 45.1%; Score 669.6; DB 7; Length 979;  
Best Local Similarity 81.6%; Pred. No. 1.3e-177;  
Matches 774; Conservative 0; Mismatches 174; Indels 0; Gaps 0;  
QY 61 TTAAAGTATTAGATGGCAGAGACATTCTCTATTACCTCAGAGTCAGTGAACGAGGACA 120

Db	24	TCAAAGATTAGAGAAATGGAGACTTCTTGTGTTCACTCTGAATCAGTCAACGAGGGACA	83
Qy	121	CCCTGACAAGCTCTCGGACCAAAATCTCCGATGCTCTCCGACGCTTGCTTGAACAGGA	180
Db	84	TCCCGACAAGCTCTCTGACCAAGGATATCCGATGCACTGCTTGACGCGCTGCTAGCTCAGGA	143
Qy	181	CCGACACAGCAAGGTTGCTCGGAAACATGCACCAAGACCAACTTGGTTCATGGTCTTGG	240
Db	144	CCCTGAAGCAAGTTGCTTTGTGAGACTTGTACCAAGACCAACTTGGTATGGTCTTTGG	203
Qy	241	AGAGATCACCAAGGCCAACGTTGACTACGAGAAGATCGTGCCTGACACCTGCAGGAA	300
Db	204	AGAGATCACCAAGGCCCAATATTTGATTATGAGAAGATTGTACGTGACACTTGCAGGA	263
Qy	301	CATCGGCTTGCTCTCAAAAGCATGTGGGACTTGATGCTGACAACTGCAAGGTCCTTGTAAA	360
Db	264	AATTGGATTGTGTGCCCTGATGTGTGGTTGGATGCTGACAAATGCGAGGGTCTTGTGAA	323
Qy	361	CATTGAGCAGCAGAGCCCTGATATTTGCCAGGGTGTGACGGCCACCTTACCAAGAACC	420
Db	324	CATTGAGCAGCAGAGCCCTGATATTTGCTCAAGGTTTCATGTGCTATTTGACTAAGCGACC	383
Qy	421	CGAGGAATCGGTGCTGGAGACAGGGTCACATGTTTGGCTATGCGACGAGCAAAACCCC	480
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Qy	481	AGAA'TTGATGTCATTGAGT'CATGTTTTCGAACTAAACTCGGTGCTGCTCACCGAGGT	540
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Qy	841	CATCATACTTACGGAGATGGGGTGCTCATGGTGGTGGTGTCTTCTCCGGGAAGGATCC	900
Db	804	CATTGACACTTACGAGGTTGGGGTGCTCATGAGGTTGGTGTCTTCTCTGGGAAGGATCC	863
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Db	864	TACCCAGGTCGACAGAGTGGAGCCTATATTGTGAGGCAAGCAGCTAAGAGCATTTGTTGC	923
Qy	961	AAGTGGACTAGCCAGAGGTTGATTTGTGCAAGTGTCTTATGCCATTTGG	1008
Db	924	CAATGGTCTTGTAGGAGGTGATTTGTTTCAGGTTTCATATGCCCATCG	971

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1	1485	100.0	1485	6	AR439797		AR439797 Sequence	
2	1064.4	71.7	1659	8	AB0623358		AB0623358 Phaseolus	
3	912.4	61.4	1173	8	AY560003		AY560003 Medicago	
4	866.8	58.4	1479	6	AR439798		AR439798 Sequence	
5	866.8	58.4	1479	8	LE8ALMSGA		Z24741 L. esculentum	
6	866.8	58.4	1526	8	BT012699		BT012699 Lycopersi	
7	864.8	58.2	1627	8	AF346306		AF346306 Lycopodium	
8	858.8	57.8	1667	8	LE8ALMSGB		Z24742 L. esculentum	
9	854	57.5	1437	8	POPSAMPDPT		M73430 Populus x g	
10	852.8	57.4	1303	8	AB041534		AB041534 Camellia	
11	852.4	57.4	1523	8	AY635050		AY635050 Solanum b	
12	850.4	57.3	1776	8	CS1277206		AT277206 Camellia	
13	849.8	57.2	7894	8	AP004964		AP004964 Lotus cor	
14	848.6	57.1	1381	8	CRGAMS2		Z71272 C. roseus mR	
15	847.6	57.1	1628	8	MCU79767		U79767 Mesembryant	
16	847.4	57.1	1886	8	AF531479		AF531479 Carica pa	
17	845.2	56.9	1531	8	AF321001		AF321001 Suaeda ma	
18	844.4	56.8	1678	8	AB183563		AB183563 Atriplex	
19	844.2	56.8	1515	8	AY259227		AY259227 Litchi ch	

Db 241 AGAGATCACCAAGGCCAAAGCTTGACTACGAGAAGATCGTGGTGACACCTGCAGGA 300  
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Qy 601 GTATTACAATGACAAACGGTGCATGTTCCAGTTCGTGTCCACACTGCTTATCTCCAC 660  
Db 601 GTATTACAATGACAAACGGTGCATGTTCCAGTTCGTGTCCACACTGCTTATCTCCAC 660  
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Db 841 CATCGATATCTTACGAGAGATGGGGTCTCATGGTGTGTGCTTTCTCCGGGAAGATCC 900  
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Qy 1381 CTGCGCTTCATTGTAATTTTTTACATGATCAACTAAAAATGTACTCTCTGTTTCCGA 1440  
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Qy 1441 CCATTGTGCTCTCTTAATATCATGATCAAAAAAGATGTTCCAAAGTT 1485  
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RESULT 2  
AB062358 1659 bp mRNA linear PLN 11-JAN-2002  
LOCUS Phaseolus lunatus SAMS mRNA for S-adenosylmethionine synthetase,  
DEFINITION complete cds.  
ACCESSION AB062358  
VERSION AB062358.1 GI:18157330  
KEYWORDS  
SOURCE Phaseolus lunatus (lima bean)  
ORGANISM Phaseolus lunatus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Phaseolus.  
1  
REFERENCE  
AUTHORS Arimura, G., Ozawa, R., Nishioka, T., Boland, W., Koch, T., Kuhnemann, F.  
and Takabayashi, J.  
TITLE Herbivore-induced volatiles induce the emission of ethylene in  
neighboring lima bean plants  
JOURNAL Plant J. 29 (1), 87-98 (2002)  
MEDLINE 22056020  
PubMed 12060229  
REFERENCE  
AUTHORS Arimura, G., Takabayashi, J. and Nishioka, T.  
TITLE Direct Submission  
JOURNAL Submitted (25-MAY-2001) Gen-ichiro Arimura, Kyoto University,  
Laboratory of Insect Physiology, Graduate School of Agriculture,  
Kitashirakawa Oiwake-cho, Sakyo-ku, Kyoto, Kyoto 606-8502, Japan  
(E-mail: arimuragokais.kyoto-u.ac.jp, Tel:81-75-753-6308,  
Fax:81-75-753-6312)

FEATURES  
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ACCESSION AR439798  
VERSION AR439798.1 GI:42665741

KEYWORDS SOURCE ORGANISM  
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AUTHORS Falco,S.C. and Allen,S.M.  
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 Espartero, J., Pintor-Toro, J.A. and Pardo, J.M.  
 Differential accumulation of S-adenosylmethionine synthetase transcripts in response to salt stress  
 Plant Mol. Biol. 25 (2), 217-227 (1994)  
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 2 (bases 1 to 1479)  
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 Differential expression of three S-adenosylmethionine synthetase genes in response to stress in tomato  
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 Pardo, J.M.  
 Direct Submission  
 Submitted (23-JUL-1993) Jose M. Pardo, Instituto de Recursos Naturales y Agrobiologia, C.S.I.C., Avda. Reina Mercedes, Sevilla, Sevilla, 41080, Spain  
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Query Match 58.4%; Score 866.8; DB 8; Length 1479;  
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ACCESSION BT012699
VERSION BT012699.1 GI:47104114
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asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
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Kirkness, E.F., Wang, W. and Vazeille, A.
Direct Submission
Submitted (11-MAY-2004) The Institute for Genomic Research, 9712
Medical Center Drive, Rockville, MD 20850, USA
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Best Local Similarity 81.5%; Pred. No. 1.2e-216;
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SOURCE      Elaeagnus umbellata
ORGANISM    Elaeagnus umbellata
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AUTHORS    Lee,S.H. and An,C.S.
TITLE      Structures and expression patterns of two cDNA clones encoding
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JOURNAL    Unpublished
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AUTHORS    Lee,S.H. and An,C.S.
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Query Match      58.2%; Score 864.8; DB 8; Length 1627;
Best Local Similarity 80.4%; Pred. No. 4.1e-216;
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QY 380 GATATTGCCAGGGTGTGACGGCCACCTTACCAAAAGACCCGAGGAAATCGGTGCTGGA 439
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DEFINITION 224742
ACCESSION  Z24742.1 GI:429105
VERSION    S-adenosyl-L-methionine synthetase.
KEYWORDS   Lycopersicon esculentum (tomato)
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ORGANISM	Lycopseisicon esculentum
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum; Lycopseisicon. 1 (bases 1 to 1667)
AUTHORS	Espartero, J., Pintor-Toro, J.A. and Pardo, J.M.
TITLE	Differential accumulation of S-adenosylmethionine synthetase transcripts in response to salt stress
JOURNAL	Plant Mol. Biol. 25 (2), 217-227 (1994)
MEDLINE	94289646
PUBMED	8018871
REFERENCE	2 (bases 1 to 1667)
AUTHORS	Espartero, J. and Pardo, J.M.
TITLE	Differential expression of three S-adenosylmethionine synthetase genes in response to stress in tomato
JOURNAL	Unpublished
REFERENCE	3 (bases 1 to 1667)
AUTHORS	Pardo, J.M.
TITLE	Direct Submission
JOURNAL	Submitted (23-JUL-1993) Jose M. Pardo, Instituto de Recursos Naturales y Agrobiologia., C.S.I.C., Avda. Reina Mercedes, Sevilla, Sevilla, 41080, Spain
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Matches	977; Conservative 0; Mismatches 197; Indels 0; Gaps 0;
QY	80 GAGACATTCCTATTTACCTCAGAGTCAGTGAACGAGGACACCCCTGACAAAGCTCTGCGAC 139
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QY	200 TCGAAACATGACCAAGACCACTTGGTCTGATGCTTCGGAGAGATCAACCAAGGCC 259
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QY	260 AACGTTGACTACGAGAAGATCGTGGCTGACACCTCGAGGAACATCGGCTTCGTCTCAAC 319
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## ORIGIN

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QY	560 CCATGGTTGAGCCCTGATGGGAAACCCCAAGTACTGTTGAGTATTAACAATGACAAACGCT 619
DB	778 TCTTGGCTTAGACCTGATGGTAAACACAAGTACTGTTGAGTATCAACAATGACAATGGT 837
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DB	838 GCTATGGTTCTCTACGTTTACACTGTTTAAATCTCCACTCAGCATGATGAGACTGTT 897
QY	680 ACCAACGACGAAATTCGACGCTCAAGGAGCATGTGATCAAGCCGCTGATCCCGGAG 739
DB	898 ACCAATGATGAATTCCTCGTGTCTCAAGAGCATGTCTCAAGCCCTGTCTATCCCGGAG 957
QY	740 AAGTACCTTGTGAGAGAACCAATTTCCACTTGAACCCCTCTGGCCGCTTTGTCTATTGGA 799
DB	958 AAGTATCTTGATGAGAACACCATTTTCCACCTCAACCCCTCAGGCCGTTTGTCTATTGGT 1017
QY	800 GGTCTCTACGGTGATGCTGCTCACCGGCGCGAAGATCATCATCGACTACTTACGGAGGA 859
DB	1018 GGACCTCACGGTGATGCTGCTCACTGGCGGTAAAGATCATCATTGACACTTACCGAGGT 1077
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DB	1198 TGCATTGTTCAGGTTTTCATATGCCATCGGTGTGCTGAGCCATTGTCGCTCTTTGTGGAC 1257
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DB	1378 TTCTTGAAGACTGTGCTTATGGCCATTTTGTAGAGATGATCTCTGACTTTCATCATGGGAA 1437
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DB	1438 GTAGTTAAGCCTCTCAAGTGGGACAAAGCCTGAAG 1471

## RESULT 9

POPSAMPDPT	POPSAMPDPT
LOCUS	Populus x generosa tissue-type leaf S-adenosyl methionine synthetase mRNA, complete cds.
DEFINITION	Populus x generosa tissue-type leaf S-adenosyl methionine synthetase mRNA, complete cds.
ACCESSION	M73430
VERSION	M73430.1
KEYWORDS	GI:497899
SOURCE	Populus balsamifera subsp. trichocarpa x Populus deltoides
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Malpighiales; Salicaceae; Populus.

REFERENCE 1 (bases 1 to 1437)  
AUTHORS Van Doorslaere,J., Gielen,J., Van Montagu,M. and Inze,D.  
TITLE A cDNA encoding S-adenosyl-L-methionine synthetase from poplar  
JOURNAL Plant Physiol. 102 (4), 1365-1366 (1993)  
MEDLINE 94105359  
PUBMED 8278561

REFERENCE 2 (bases 1 to 1437)  
AUTHORS Van Montagu,M.  
TITLE Direct Submission  
JOURNAL Submitted (15-JUL-1991) M. Van Montagu, Laboratorium voor Genetica,  
Universiteit Gent, K.L. Ledeganckstraat 35, B-9000 Gent, Belgium  
COMMENT On Jun 6, 1994 this sequence version replaced gi:169464.  
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ORIGIN

Query Match 57.5%; Score 854; DB 8; Length 1437;  
Best Local Similarity 83.0%; Pred. No. 2.8e-213;  
Matches 974; Conservative 0; Mismatches 200; Indels 0; Gaps 0;

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QY 192 AGTTCCTCGGAAACATGCAACCAACCACTTGCTCATGTCTTCGAGAGATCACCA 251  
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RESULT 10  
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LOCUS  
DEFINITION  
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complete cds.  
ACCESSION  
AB041534  
VERSION  
AB041534.1 GI:7594740  
KEYWORDS  
s-adenosylmethionine synthetase.  
SOURCE  
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ORGANISM  
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REFERENCE  
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AUTHORS  
Feng, Y.F. and Liang, Y.R.  
TITLE  
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JOURNAL  
Published Only in Database (2000)  
REFERENCE  
2 (bases 1 to 1303)  
AUTHORS  
Feng, Y.F. and Liang, Y.R.  
TITLE  
Direct Submission  
JOURNAL  
Submitted (09-APR-2000) Yan F. Feng, Tea Department Hua Jia Chi  
Campus Zhe Jiang Uni., Tea Department; 268 Kai Xuan Road, Hang zhou  
310029, China (E-mail:yf01@yahoo.com, Tel:81-5716971704,  
Fax:81-5716971704)  
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ORIGIN
Query Match 57.4%; Score 852.8; DB 8; Length 1303;
Best Local Similarity 82.8%; Pred. No. 5.6e-213;
Matches 985; Conservative 0; Mismatches 203; Indels 1; Gaps 1;

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DB 251 GATGTGGTCTTGATGCTGATTAATGCAAGGTTCTAGTCAAATCGAGCAACAGAGCCCT 310
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QY 1160 TTCTTGAAGACTGCTGCATATGACATTCGCGCAGAGAGGACCTGACTTCACATGGG-A 1218
DB 1091 TTCTTGAAGACTGCTGCCTATGACATTTTGGCAGGATGATCTGACTTCACATGGGA 1150
QY 1219 AGTGGTCAAGCCCTCAAGTGGGAGAGGCTCAAGGCCATTCATTCCAC 1267
DB 1151 AGTGGTGAAGCCCTCAAGTGGGACAAACCTCAAGCTAATTTCTTCCCGC 1199

RESULT 11
AY635050 1523 bp mRNA linear PLN 23-JUN-2004
LOCUS Solanum brevifolium S-adenosyl methionine synthase mRNA, complete
cDS.
ACCESSION AY635050
VERSION AY635050.1 GI:48928009
KEYWORDS
SOURCE
ORGANISM Solanum brevifolium
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum.
REFERENCE
AUTHORS Seo, H.W., Yi, J.Y., Moon, J.Y., Park, Y.E. and Cho, J.H.
TITLE SAM and polyamine levels in transgenic tomato fruits and potato
tuber with SAM synthase gene
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1523)
AUTHORS Seo, H.W., Yi, J.Y., Moon, J.Y., Park, Y.E. and Cho, J.H.
TITLE Direct Submission
JOURNAL Submitted (25-MAY-2004) National Institute of Highland Agriculture,
Hoengse 3ri Doam Pyongchang, Gangwon 232 - 955, South Korea
FEATURES
source
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109..1290
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IPEKYDEKTIIFHLNPSGRFVIGPHGDAGLTGRKIIIDTYGGWGAHGGAFSGKDP"
CDS
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KVDRSGAYIVROAAKSIIVASGLARRCIIVQVSAIVGPEPLSVFVDTYGTGKIPDREIL  
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D"

ORIGIN		Query Match		57.4%; Score 852.4; DB 8; Length 1523;	
		Best Local Similarity		78.3%; Pred. No. 7.3e-213;	
		Matches 1035; Conservative		0; Mismatches 286; Indels 1; Gaps 1;	
QY	80	GAGACATTCCTATTTACCTCAGAGTCAGTGAACGAGGAGACACCCTCAGCAAGCTCTCGGAC	139		
DB	112	GAACCTTTCTATTCACCTCCGAGTCTGTGAACGAGGTCACCCAGCAAGCTCTCTGTAT	171		
QY	140	CAAAATCTCCGATCTGTCTCGACGCTTGCTTGAACAGSACCAGACGACGAAGGTGGC	199		
DB	172	CAGATCTCTGATCGAGTCTTGATGCTGCTTGAGCAAGATCTCTGAGACGAAGTTGCA	231		
QY	200	TGGGAACATGACCAAGACCAACTTGGTCATGGTCTTCGGAGAGATCACCAAGGCC	259		
DB	232	TGTGAAACTTGCACCAAGACCAACTTGGTCATGGTCTTCGGTGAATCAACCAAGGCT	291		
QY	260	AACGTTGACTACGAGAAAGATCGTGCCTGACACCTGCAGGAACATCGGCTTCGTCTCAAC	319		
DB	292	ATTGTAGACTATGAGAAATCGTGCCTGACACATGCGGTAACTTGGATTTGTTCTGAT	351		
QY	320	GATGTGGACTTGATCTGACAACTGCAAGGCTCTTGTAAACATTTGAGCAGCAGCCCT	379		
DB	352	GATGTTGGTCTTGATCGCGACAACTGCAAGGCTCTTGTAACTTGGATTTGTTCTGAT	411		
QY	380	GATATTTGCCAGGCTGTGACGGCCACCTTACAAAGACCCGAGGAATCGTGTCTGA	439		
DB	412	GATATTTGCTCAAGGCTGTGACGGCCACTGACCAACCGCCCTGAGGAGATTTGTTGCTGT	471		
QY	440	GACCAAGGTCACATGTTTGGCTATGCCAGCGAAGCCCAAGATTTGATGCAATTTGAT	499		
DB	472	GACCAAGGTCACATGTTTGGCTATGCCAGCGAAGCCCAAGATTTGATGCAATTTGAT	531		
QY	500	CATGTTCTTTCGCAACTAACTCGTGTCTCTCACCGAGGTTTCGCAAGACCGAACCTGC	559		
DB	532	CAGTGTCTTTCGCAACTAACTCGTGTCTCTCACCGAGGTTTCGCAAGACCGAACCTGC	591		
QY	560	CAATGTTGAGGCTGATGGGAAACCCCAAGTGAATGTTGAGTATTAATGACACAGGT	619		
DB	592	CGTGTGTTGAAGCTGATGGCAAACTCAAGTTACTGTTGAGTACTGCAATGACATGTT	651		
QY	620	GCATGTTTCCAGTTCGTGTGCACACTGTCTTATCTCCACCCCAACATGATGAGCTGT	679		
DB	652	GCCATGATTCATTTAGGCTGCACACTGTTCTCATCTCCACTCAACACGATGAGACTGTT	711		
QY	680	ACCAACGAGAAATTCGAGTGCACCTCAAGGAGCATGTGATCAAGCGGTGATCCCGGAG	739		
DB	712	ACAAATGATGAGATTCGCCCGACCTTAAGGAGCATGCTATCAAGCCAGTCAATCCAGAG	771		
QY	740	AAGTACCTTGATGAGAAACCAATTTTCACCTTGAACCCCTCTGGCGGTTTGTGATGGA	799		
DB	772	AAGTACCTTGATGAGAAACCAATTTTCACCTTGAACCCCTCTGGCGGTTTGTGATGGA	831		
QY	800	GGTCTCACGTTGATGCTGTCTCACCGCCGACAGATCATCATGATCTTACGAGGA	859		
DB	832	GGACCTCATGGTGTGCTGTCTCACCGCCGACAGATCATCATGATCTTACGAGGA	891		
QY	860	TGGGTGCTCATGGTGTGCTGTCTCACCGGAGGATTCACCAAGGTTGATAGGAGT	919		
DB	892	TGGGTGCCCATGGTGTGCTGTGATCTCTGCGAAGGACCCCAAGGTTGACAGGAT	951		
QY	920	GGTCTTACATTTGTGAGACAGGCTGTGATGAGCATTTGTGGCAAGTGAATGACGAAG	979		
DB	952	GGTGATATATTTGAAGGAGGCTGCAAGAGATTTGTAGCTAGTGTGCTGCTGCCAGA	1011		
QY	980	TGCATGTGCAAGTGTCTTATGCAATTTGCTGTGCGCGAGCCTTCTGCTCTTCTGTGAC	1039		
DB	1012	TGCATGTGCAAGTGTCTTATGCAATTTGCTGTGCGCGAGCCTTCTGCTGTGCTGTGAC	1071		

QY	1040	ACCTATGCGACCGGAGGATCCATGATAGGAGATTTCAACATTTGTGAAGGAGAACTTT	1099		
DB	1072	ACCTATGCGACCTGGAAGATCCCGACAGGGAATTTTGAAGATCGTTAAGGAGAACTTC	1131		
QY	1100	GATTTTCAGGCGGATGATCTCCATCAACCTTTGATCTCAAGAGGGTGGGATAACAGG	1159		
DB	1132	GACTTCAGACCTGGAATGATGTCATTAACCTTGGATTTGAAGAGGGTGGCAATGGAGA	1191		
QY	1160	TTCTTTGAAGACTGCTGCATATGACACCTTCGCGACAGAGGACCCCTGACCTTCACATGG	1219		
DB	1192	TTCTTTGAAGACTGCTGCCTATGCTCATTTTGGACGCGACGCTGATTTTCAATGGAA	1251		
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DB	1252	GTGTCAGAGCCCTCAAGTGGGAGAGGCTTAAGCCATTCATTCACGCAATGTGCTG	1311		
QY	1280	GGAGTTTTCAGGCTTGCCTTATATGCTATATTCATATTCACATCTTCCAGCTCCCTGCT	1339		
DB	1312	CTATGTTTTCCTTCTTCTTGTGCTTGTGCTTTTGAATCCCTGCTGTTGCTGCT	1371		
QY	1340	CTGTCGCTTTTCTCTGCTGCTCTCTCTATTTTGTCTCTCTGCTCTTTCATTTGTAAT	1398		
DB	1372	CTATGATTTTCTCTTTTTCACCTTTTTCGCTATTTGCTGCTTCCATTTGTTGGAAC	1431		
QY	1399	TT 1400			
DB	1432	TT 1433			

RESULT 12  
CS1277206 1776 bp DNA linear PLN 28-MAR-2000  
LOCUS  
Camellia sinensis gene for s-adenosylmethionine synthetase.  
DEFINITION  
AJ277206  
VERSION  
AJ277206.1 GI:7340730  
KEYWORDS  
s-adenosylmethionine synthetase.  
SOURCE  
Camellia sinensis  
ORGANISM  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; Ericales; Theaceae; Camellia.  
REFERENCE  
1  
Feng, Y.F. and Liang, Y.R.  
Cloning of s-adenosylmethionine synthetase gene in tea plant  
Unpublished  
REFERENCE  
2 (bases 1 to 1776)  
Feng, Y.F.  
Direct Submission  
Submitted (27-MAR-2000) Feng Y.F., Tea Department, Hua jia chi  
Campus, Zhe jiang University, 310029, CHINA  
FEATURES  
Location/Qualifiers  
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113..1294  
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KVDRSGAYIVROAAKSIIVASGLARRCIIVQVSAIVGPEPLSVFVDTYGTGKIPDK  
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S"

ORIGIN

Query Match 57.3%; Score 850.4; DB 8; Length 1776;





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QY 333 ATGCTGACAACTCAAGTCTCTTGTAAACATTGAGCAGCAGCCCTGATATTATGCCCAG 392
Db 545 ATGCTGACAAATGCAAGTCTTGTGTAACATTGAGCAGCAGCCCTGATATTATGCTCAG 604
QY 393 GTGTGACGCGCCACTTACCAAAAGACCGGAGAAATCGGTGCTGGAGACCAAGGTTCACA 452
Db 605 GTGTGATGCGCACTTACCAAGCGCTTGAGACATTGGTGTGCGGACCAAGGTTCACA 664
QY 453 TGTTCGCTATGCGACGAGCAACCCGAGAAATGATGCAATGATGATGATGATGATGCA 512
Db 665 TGTTCGCTATGCAATGATGAGACCCCTGAGCTCATGCCACTGAGCCATGCTCTTCGCA 724
QY 513 CTAACATCGGTGCTGCTCAGCGAGTTCGCAAGAACGGAACCTCCCATGTTGAGGC 572
Db 725 CCAACTAGAGGTAACACTCACTGAGTGTAGGAGAAATGTTACTCTGCTTGGCTGAGGC 784
QY 573 CTGATCGGAAACCCCAAGTGACTGTTGAGTATTAATGACCAACGCTGCCATGTTCCAG 632
Db 785 CCGATGCGAAGACACAAGTCAACCTTGAGTACTACAATGAGAAGCGGTGATGTTCCAG 844
QY 633 TTGCTGTCACACTGCTTATCTCACCACCAACATGATGAGACTGTGACCAAGCAAAA 692
Db 845 TTGCTGTCACACTGCTTATCTCACCACCAACATGATGAGACTGTGACCAATGACAAA 904
QY 693 TTCAGCTGACCTCAAGGAGCATGTATCAAGCGGTGATCCGGAAGAGTACTTGTATG 752
Db 905 TTGCTGCTGATCTTAAGAGGATGTATCAAGCTGTATCCCTGAGAAAGTACTTGATG 964
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Db 965 AGAAGACTATCTTCCACCTTAACCTTCAGCGCGCTTTGTCAATGTTGGCCCTCACGGCG 1024
QY 813 ATGCTGCTCACCGCGCGCAAGATCATCATGATGATCTTACGGAGAGTGGGTGCTCATG 872
Db 1025 ATGCTGCGCTTAACCGGAAGAGATCATCATGATGATCTTATGTTGGCTGGGGTGCATG 1084
QY 873 GTGGTGGTCTTCTCCGGAAGGATCCCAACCAAGGTTGATAGGAGTGTGCTTACATG 932
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QY 933 TGAGACAGGTGCTGAAGAGCATTTGTGCAAGTGGACTACCGAAGGTGCATTTGTCAAG 992
Db 1145 TGAGGCGAGCAGCAAGAGATTGTTGGCAACCGCTTAGCCGAGGTGCTTGTTCAGG 1204
QY 993 TGTCTTATGCAATGTTGCTGCGCGAGCTTTGCTGCTCTTTGTTGACCTATGACCG 1052
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QY 1053 GGAAGATCCATGATGAAGGAGATTCTCAACATTGTGAAGGAGAACTTTGATTTTCA 1112
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QY 1113 GTATGATCTCCATCAACCTTGTATCTCAAGAGGGGTGGGAATAACAGGTTCTTTGA 1172
Db 1325 GAATGATGACCATCAACTTGGACCTTTAAGAGGGGTG---AAACAGTTTCATCAAGAC 1381
QY 1173 CTGCATATGACACTTCCGCGAGAGGACCTTGACTTCACTGGGAAGTGGTCAAGCCCC 1232
Db 1382 CTGCATATGACACTTTGGAAGGGATGACCCAGACTTCCACTGGGAAGTTGTGAAGCCAC 1441
QY 1233 TCAAGTGGGAGAGGCTTAAG 1253
Db 1442 TCAAGTGGGAGAGCCTCAAG 1462
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RESULT 14  
CRSAMS2  
LOCUS  
DEFINITION  
ACCESSION

CRSAMS2 1381 bp mRNA linear PLN 12-FEB-1997  
C.roseus mRNA for S-adenosyl-L-methionine synthetase 2.  
271272

VERSION  
KEYWORDS  
SOURCE  
ORGANISM

271272.1 GI:1655577  
methionine adenosyltransferase; S-adenosyl-L-methionine synthetase.  
Catharanthus roseus (Madagascar periwinkle)  
Catharanthus roseus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;  
asterids; lamids; Gentianales; Apocynaceae; Rauvolfioideae;  
Vinceae; Catharanthus.  
1 (bases 1 to 1381)  
Schroder, G., Eichel, J., Breinig, S. and Schroeder, J.  
Three differentially expressed S-adenosylmethionine synthetases  
from Catharanthus roseus: molecular and functional characterization  
Plant Mol. Biol. 33 (2), 211-222 (1997)  
97188555  
9037140

REFERENCE  
AUTHORS  
TITLE

JOURNAL  
MEDLINE  
PUBMED

REFERENCE  
AUTHORS  
TITLE

JOURNAL  
REFERENCE  
AUTHORS  
TITLE

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JOURNAL  
AUTHORS  
TITLE

FEATURES  
source

gene

CDS

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Ppi + Pi"  
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A"

ORIGIN

Query Match 57.1%; Score 848.6; DB 8; Length 1381;  
Best Local Similarity 80.3%; Pred. No. 7.2e-212;  
Matches 995; Conservative 0; Mismatches 244; Indels 0; Gaps 0;  
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Db 6 CTCGATTTCTCTCGTTGCTCTGCCCTGCTCCATCTGTCTACCGCAAGTTTAGAAGGAT 65  
QY 79 AGAGACATTCCTATTATTCCTCAGAGTCAGTGAAACGAGGACACCTCTGACAGCTTCGCA 138  
Db 66 GGAGACCTTTTGTTCACATCTGAGTCGCTGAATGAGGACACCTCTGATAGCTTTGTA 125  
QY 139 CCAATCTCCGATGCTGCTCGAGCTTCCCTTGAACAGGACCCAGACAGCAAGGTTGC 198  
Db 136 CGAGATCTCAGATGAGTGCTAGTGCCTGTTTAGCAGGACCTCTGAGACAGGTTGC 185





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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 30, 2005, 18:40:09 ; Search time 816.183 Seconds  
(without alignments)  
10770.640 Million cell updates/sec

Title: US-10-734-698A-38  
Perfect score: 1485  
Sequence: 1 AGCCAGGCCCACTCAACCA.....CAAAAGATGTTCCAGTT 1485

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues 8780412  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : N Geneseq\_16Dec04:\*  
1: Geneseqn1980s:\*  
2: Geneseqn1990s:\*  
3: Geneseqn2000s:\*  
4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002as:\*  
7: Geneseqn2002bs:\*  
8: Geneseqn2003as:\*  
9: Geneseqn2003bs:\*  
10: Geneseqn2003cs:\*  
11: Geneseqn2003ds:\*  
12: Geneseqn2004as:\*  
13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1485	100.0	1485	2	AAX07184 Soybean S
2	1485	100.0	1518	3	AA51037 Soybean S
3	824.2	55.5	1529	3	AAC33535 Arabidops
4	822.8	55.4	1190	8	ADA69525 Rice gene
5	819.8	55.2	1191	12	ADJ44928 Plant cDN
6	819.6	55.2	1582	2	AAX07183
7	813.4	54.8	1190	8	ADA70676 Rice gene
8	804.4	54.2	1521	3	AAC45478 Arabidops
9	802.8	54.1	1508	3	AAC33986 Arabidops
10	796.4	53.6	1182	8	ADA67853 Arabidops
11	796.4	53.6	1393	3	AAC46421 Arabidops
12	786.4	53.0	1182	2	AAT99141
13	786.4	53.0	1185	8	ADA69780 Rice gene
14	783.6	52.8	1395	3	AAC33674 Arabidops
15	778.6	52.4	1182	2	AAT99143
16	777.8	52.4	1380	2	AAX07185 Wheat S-a
17	777	52.3	1182	2	AAT99142
18	755.2	50.9	1674	3	AAC47744 Zea mays
19	745.2	50.2	1636	5	AAD02296 Nicotiana
20	729.2	49.1	1173	6	AB214640 Arabidops

21	729.2	49.1	1653	3	AAC45944 Arabidops
22	715.6	48.2	1654	3	AAC35348 Arabidops
23	468.4	31.5	725	9	ACL15153 DNA clone
24	458.8	30.9	622	13	ACN49337 Cotton pr
25	458.2	30.9	710	9	ACL15154 DNA clone
26	457.2	30.8	618	13	ACN50650 Cotton an
27	443.8	29.9	522	3	AAA51039 Partial s
28	427	28.8	1185	13	ADSL17323 Rat liver
29	422.8	28.5	676	9	ACL15152 DNA clone
30	422.4	28.4	2801	12	ADQ84785 Human tum
31	422.4	28.4	2828	10	ADG32724 Human DNA
32	422.4	28.4	2828	12	ADJ74787 Marker ge
33	422.4	28.4	2828	12	ADJ19098 Human PRO
34	422.4	28.4	2828	12	ADO19096 Human PRO
35	422.4	28.4	2828	13	ADQ91617 Human met
36	422.4	28.4	2828	13	ACN37730 Tumour-as
37	420.8	28.3	1283	5	AAC91225 Human met
38	420.8	28.3	1283	11	AD132045 Human CDN
39	419.6	28.3	3495	12	ADL12741 Human ste
C 40	419.2	28.2	672	9	ACL15221 DNA clone
C 41	419.2	28.2	617	9	ACL15210 DNA clone
C 42	418.8	28.2	1840	10	ADB59179 Toxicity-
C 43	418.8	28.2	1840	10	ADB53879 Primary r
C 44	416.6	28.1	631	9	ACL15198 DNA clone
C 45	414.4	27.9	623	9	ACL15211 DNA clone

ALIGNMENTS

RESULT 1  
AAX07184  
ID AAX07184 standard; CDNA; 1485 BP.  
XX  
AC AAX07184;  
XX

DT 21-MAY-1999 (first entry)  
XX

DE Soybean S-adenosylmethionine synthetase cDNA clone s2.12b06.  
XX

KW S-adenosylmethionine synthetase; soybean; amino acid; lysine; threonine;  
KW methionine; cysteine; isoleucine; transgenic plant; crop improvement;  
KW food; feedstuff; ss.  
XX

OS Glycine max.  
XX

XX  
FH Key Location/Qualifiers  
FT CDS 74..1252  
FT /tag= a  
XX

XX W09855601-A2.  
XX

PD 10-DEC-1998.  
XX

XX 05-JUN-1998; 98WO-US011692.  
XX

PR 06-JUN-1997; 97US-0048771P.  
PR 12-JUN-1997; 97US-0049443P.  
XX

XX (DUPO ) DU PONT DE NEMOURS & CO E I.  
XX  
XX Falco SC, Allen SM, Rafaleski JA, Hitz WD, Kinney AJ, Abell LM;  
XX Thorpe CJ;  
XX

XX WPI, 1999-070263/06.  
XX P-PSDB; AAW97743.  
XX

XX New plant amino acid biosynthetic enzymes, DNA and chimeric genes -  
XX PT encode: dihydropicolinate reductase; diaminopimelate epimerase; threonine  
XX synthase; threonine deaminase; S-adenosylmethionine synthetase.  
XX  
XX Claim 44; Page 66-67; 99pp; English.  
XX



FT CDS /\*tag= a  
FT 74..1252  
FT /\*tag= b  
FT /product= "S-adenosyl-L-methionine\_Synthetase"  
XX  
XX WO200037662-A2.  
XX  
XX 29-JUN-2000.  
XX  
XX 17-DEC-1999; 99WO-US030180.  
XX  
XX 21-DEC-1998; 98US-0113045P.  
XX  
XX (DUPO ) DU PONT DE NEWMOURS & CO E. I.  
XX  
XX Falco SC, Li Z;  
XX  
XX WPI; 2000-442682/38.  
XX

S-adenosyl-L-methionine synthetase promoter for expressing target  
PT heterologous herbicide-resistance or pathogen-resistance nucleic acid  
PT fragments in plants, especially soybean.  
XX  
XX Example 2; Page 39; 50pp; English.

CC This is the soybean full-length S-adenosyl-L-methionine synthetase (SAMS)  
CC cDNA, which was used to generate a probe to isolate a SAMS promoter. The  
CC SAMS promoter is active in seedlings and callus and over-expression of a  
CC gene in embryo stage can be achieved at an early developing stage using  
CC the SAMS promoter. The SAMS promoter may be used as an alternative to  
CC cauliflower mosaic virus 35S promoter to drive expression of selectable  
CC marker genes. Plant cells transformed with the SAMS constitutive promoter  
CC are useful for increasing or decreasing the expression of heterologous  
CC nucleic acid fragments in a plant, preferably corn, rice, wheat, barley,  
CC palm, Arabidopsis, soybean, oil seed Brassica, peanut, sunflower,  
CC safflower, cotton, tobacco, tomato, potato or cocoa. Target heterologous  
CC nucleic acid fragments include herbicide or pathogen resistance nucleic  
CC acid fragments

SQ Sequence 1518 BP; 399 A; 373 C; 357 G; 389 T; 0 U; 0 Other;

Query Match 100.0%; Score 1485; DB 3; Length 1518;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	421	CGAGGAAATCGGTGCTGGAGACGAGGTCAATGTTTGGCTATGCCACGGAAGAAACCCC	480
DB	421	CGAGGAAATCGGTGCTGGAGACGAGGTCAATGTTTGGCTATGCCACGGAAGAAACCCC	480
QY	481	AGAAATTGATGCCATTGAGTCATGTTCTTGCACAACTCGGTGCTCGTCTCACCGAGGT	540
DB	481	AGAAATTGATGCCATTGAGTCATGTTCTTGCACAACTCGGTGCTCGTCTCACCGAGGT	540
QY	541	TCGCAAGAACGGAACCTGCCATGTTGAGGCTGATGGGAAACCAAGTACTGTGTA	600
DB	541	TCGCAAGAACGGAACCTGCCATGTTGAGGCTGATGGGAAACCAAGTACTGTGTA	600
QY	601	GTATTACAATGACACGCTGCCATGTTCCAGTTCGTGTCACACTGTGTTATCTCCAC	660
DB	601	GTATTACAATGACACGCTGCCATGTTCCAGTTCGTGTCACACTGTGTTATCTCCAC	660
QY	661	CCAAATGATGAGACTGTGACCAACGACCAATTCAGCTGACCTCAAGGAGCATGTAT	720
DB	661	CCAAATGATGAGACTGTGACCAACGACCAATTCAGCTGACCTCAAGGAGCATGTAT	720
QY	721	CAAGCCGCTGATCCCGGAGAGTACCTTGATGAGAGACCAATTTTCCACTTGAACCCCTC	780
DB	721	CAAGCCGCTGATCCCGGAGAGTACCTTGATGAGAGACCAATTTTCCACTTGAACCCCTC	780
QY	781	TGCGCGTCTTGTGATTTGAGAGTCTTCAACGCTGATGCTGCTCAACGCGCGCAAGATCAT	840
DB	781	TGCGCGTCTTGTGATTTGAGAGTCTTCAACGCTGATGCTGCTCAACGCGCGCAAGATCAT	840
QY	841	CATCGATCTTACGAGGATGGGTGCTCATCGTGGTGGTGGTCTTCTCCGGGAGGATCC	900
DB	841	CATCGATCTTACGAGGATGGGTGCTCATCGTGGTGGTGGTCTTCTCCGGGAGGATCC	900
QY	901	CACCAAGGTTGATAGAGTGGTGTTCATCTTGACAGACAGGCTGCTAAGAGCATTTGGC	960
DB	901	CACCAAGGTTGATAGAGTGGTGTTCATCTTGACAGACAGGCTGCTAAGAGCATTTGGC	960
QY	961	AAGTGGACTAGCAGAGGTGATTTGCAAGTGTCTTATGCCATTTGGTGTGCCGAGCC	1020
DB	961	AAGTGGACTAGCAGAGGTGATTTGCAAGTGTCTTATGCCATTTGGTGTGCCGAGCC	1020
QY	1021	TTTGTCTGTCTTTGTGACACCTATGGCACCGGAGAGTCCATGATAGGAGATTTCTCAA	1080
DB	1021	TTTGTCTGTCTTTGTGACACCTATGGCACCGGAGAGTCCATGATAGGAGATTTCTCAA	1080
QY	1081	CATTGTGAAGAGAACTTTGATTTTCAAGCCCGGTATGATCTCCATCAACTTTGATCTCAA	1140
DB	1081	CATTGTGAAGAGAACTTTGATTTTCAAGCCCGGTATGATCTCCATCAACTTTGATCTCAA	1140
QY	1141	GAGGGTGGGAATAACAGGTTCTTGAAGACTGCTGCATATGACACTTCGGCAGAGAGGA	1200
DB	1141	GAGGGTGGGAATAACAGGTTCTTGAAGACTGCTGCATATGACACTTCGGCAGAGAGGA	1200
QY	1201	CCCTGACTTCACTGGAGTGGTCAAGCCCTCAAGTGGGAGAGGCTTAAGGCCATTC	1260
DB	1201	CCCTGACTTCACTGGAGTGGTCAAGCCCTCAAGTGGGAGAGGCTTAAGGCCATTC	1260
QY	1261	ATTTCACCTGCAATGTCTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	1320
DB	1261	ATTTCACCTGCAATGTCTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	1320
QY	1321	ACTTTCCAGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1380
DB	1321	ACTTTCCAGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1380
QY	1381	CTGCGCTTCACTTTGTAATTTTATCATGATCACTTAAATAATGTAATCTCTGTTTCCGA	1440
DB	1381	CTGCGCTTCACTTTGTAATTTTATCATGATCACTTAAATAATGTAATCTCTGTTTCCGA	1440
QY	1441	CCATTGTGTCTCTTAATATCAGTATCAAAAGAAATGTTTCCAAAGTT	1485
DB	1441	CCATTGTGTCTCTTAATATCAGTATCAAAAGAAATGTTTCCAAAGTT	1485

RESULT 3  
AAC33535  
ID AAC33535 standard; DNA; 1529 BP.  
XX  
AC AAC33535;  
XX  
DT 17-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 3408.  
XX  
KW Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway; metabolic pathway;  
KW promoter; termination sequence; ss.  
XX  
OS Arabidopsis thaliana.  
XX  
PN EP1033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-00301439.  
XX  
PR 25-FEB-1999; 99US-0121825P.  
PR 05-MAR-1999; 99US-0123180P.  
PR 09-MAR-1999; 99US-0123548P.  
PR 23-MAR-1999; 99US-0125788P.  
PR 25-MAR-1999; 99US-0126264P.  
PR 29-MAR-1999; 99US-0126785P.  
PR 01-APR-1999; 99US-0127462P.  
PR 06-APR-1999; 99US-0128234P.  
PR 08-APR-1999; 99US-0128714P.  
PR 16-APR-1999; 99US-0129845P.  
PR 19-APR-1999; 99US-0130077P.  
PR 21-APR-1999; 99US-0130449P.  
PR 23-APR-1999; 99US-0130510P.  
PR 23-APR-1999; 99US-0130891P.  
PR 28-APR-1999; 99US-0131449P.  
PR 30-APR-1999; 99US-0132048P.  
PR 30-APR-1999; 99US-0132407P.  
PR 04-MAY-1999; 99US-0132484P.  
PR 05-MAY-1999; 99US-0132485P.  
PR 06-MAY-1999; 99US-0132486P.  
PR 06-MAY-1999; 99US-0132487P.  
PR 07-MAY-1999; 99US-0132863P.  
PR 11-MAY-1999; 99US-0134256P.  
PR 14-MAY-1999; 99US-0134218P.  
PR 14-MAY-1999; 99US-0134219P.  
PR 14-MAY-1999; 99US-0134221P.  
PR 14-MAY-1999; 99US-0134370P.  
PR 18-MAY-1999; 99US-0134768P.  
PR 19-MAY-1999; 99US-0134941P.  
PR 20-MAY-1999; 99US-0135124P.  
PR 21-MAY-1999; 99US-0135353P.  
PR 24-MAY-1999; 99US-0135629P.  
PR 25-MAY-1999; 99US-0136021P.  
PR 27-MAY-1999; 99US-0136392P.  
PR 28-MAY-1999; 99US-0136782P.  
PR 01-JUN-1999; 99US-0137222P.  
PR 03-JUN-1999; 99US-0137528P.  
PR 04-JUN-1999; 99US-0137502P.  
PR 07-JUN-1999; 99US-0137724P.  
PR 08-JUN-1999; 99US-0138094P.  
PR 10-JUN-1999; 99US-0138540P.  
PR 10-JUN-1999; 99US-0138847P.  
PR 14-JUN-1999; 99US-0139119P.  
PR 16-JUN-1999; 99US-0139452P.  
PR 16-JUN-1999; 99US-0139453P.  
PR 17-JUN-1999; 99US-0139492P.  
PR 18-JUN-1999; 99US-0139454P.  
PR 18-JUN-1999; 99US-0139455P.  
PR 18-JUN-1999; 99US-0139456P.  
PR 18-JUN-1999; 99US-0139457P.  
PR 18-JUN-1999; 99US-0139458P.  
PR 18-JUN-1999; 99US-0139459P.  
PR 18-JUN-1999; 99US-0139460P.  
PR 18-JUN-1999; 99US-0139461P.  
PR 18-JUN-1999; 99US-0139462P.  
PR 18-JUN-1999; 99US-0139463P.  
PR 18-JUN-1999; 99US-0139750P.  
PR 18-JUN-1999; 99US-0139763P.  
PR 21-JUN-1999; 99US-0139817P.  
PR 22-JUN-1999; 99US-0139899P.  
PR 23-JUN-1999; 99US-0140353P.  
PR 23-JUN-1999; 99US-0140354P.  
PR 24-JUN-1999; 99US-0140695P.  
PR 28-JUN-1999; 99US-0140823P.  
PR 29-JUN-1999; 99US-0140991P.  
PR 30-JUN-1999; 99US-0141287P.  
PR 01-JUL-1999; 99US-0141842P.  
PR 01-JUL-1999; 99US-0142154P.  
PR 02-JUL-1999; 99US-0142055P.  
PR 06-JUL-1999; 99US-0142390P.  
PR 08-JUL-1999; 99US-0142803P.  
PR 09-JUL-1999; 99US-0142920P.  
PR 12-JUL-1999; 99US-0142977P.  
PR 13-JUL-1999; 99US-0143542P.  
PR 14-JUL-1999; 99US-0143624P.  
PR 15-JUL-1999; 99US-0144005P.  
PR 16-JUL-1999; 99US-0144085P.  
PR 16-JUL-1999; 99US-0144086P.  
PR 19-JUL-1999; 99US-0144325P.  
PR 19-JUL-1999; 99US-0144331P.  
PR 19-JUL-1999; 99US-0144332P.  
PR 19-JUL-1999; 99US-0144333P.  
PR 19-JUL-1999; 99US-0144334P.  
PR 19-JUL-1999; 99US-0144335P.  
PR 20-JUL-1999; 99US-0144352P.  
PR 20-JUL-1999; 99US-0144632P.  
PR 20-JUL-1999; 99US-0144884P.  
PR 21-JUL-1999; 99US-0144814P.  
PR 21-JUL-1999; 99US-0145086P.  
PR 21-JUL-1999; 99US-0145088P.  
PR 22-JUL-1999; 99US-0145085P.  
PR 22-JUL-1999; 99US-0145087P.  
PR 22-JUL-1999; 99US-0145089P.  
PR 22-JUL-1999; 99US-0145192P.  
PR 23-JUL-1999; 99US-0145145P.  
PR 23-JUL-1999; 99US-0145218P.  
PR 23-JUL-1999; 99US-0145224P.  
PR 26-JUL-1999; 99US-0145276P.  
PR 27-JUL-1999; 99US-0145913P.  
PR 27-JUL-1999; 99US-0145918P.  
PR 27-JUL-1999; 99US-0145919P.  
PR 28-JUL-1999; 99US-0145951P.  
PR 02-AUG-1999; 99US-0146386P.  
PR 02-AUG-1999; 99US-0146388P.  
PR 02-AUG-1999; 99US-0146389P.  
PR 03-AUG-1999; 99US-0147038P.  
PR 04-AUG-1999; 99US-0147204P.  
PR 04-AUG-1999; 99US-0147302P.  
PR 05-AUG-1999; 99US-0147192P.  
PR 05-AUG-1999; 99US-0147260P.  
PR 06-AUG-1999; 99US-0147303P.  
PR 06-AUG-1999; 99US-0147416P.  
PR 09-AUG-1999; 99US-0147493P.  
PR 09-AUG-1999; 99US-0147935P.  
PR 10-AUG-1999; 99US-0148171P.  
PR 11-AUG-1999; 99US-0148319P.  
PR 12-AUG-1999; 99US-0148341P.  
PR 13-AUG-1999; 99US-0148565P.  
PR 13-AUG-1999; 99US-0148684P.  
PR 16-AUG-1999; 99US-0149368P.  
PR 17-AUG-1999; 99US-0149175P.  
PR 18-AUG-1999; 99US-0149428P.  
PR 20-AUG-1999; 99US-0149722P.  
PR 20-AUG-1999; 99US-0149723P.





```
Db      1392 TTTGTTTATGATCATTTGTTACTTGAGCTATTTCAATTGGGTGTTGTTTATGGCGAC 1451
Qy      1400 TTTTACATG 1408
Db      1452 TTTTACAGC 1460

RESULT 4
ID      ADA69525 standard; DNA; 1190 BP.
XX
AC      ADA69525;
XX
DT      20-NOV-2003 (first entry)
XX
DE      Rice gene, SEQ ID 2848.
XX
KW      Plant; bacterial infection; fungal infection; viral infection; rice;
KW      gene; ds.
XX
OS      Oryza sativa.
XX
PN      WO2003000898-A1.
XX
PD      03-JAN-2003.
XX
PF      22-JUN-2001; 2001WO-IB001105.
XX
PR      22-JUN-2001; 2001WO-IB001105.
XX
PA      (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
PI      Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
PI      Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
XX      WPI; 2003-175290/17.
XX
PT      Identifying at least one gene involved in plant resistance or response to
PT      pathogenic infection for conferring resistance or tolerance to a plant
PT      bacterial, fungal or viral infection by determining or detecting plant
PT      gene expression.
XX
PS      Claim 6; SEQ ID NO 2848; 899pp; English.
XX
CC      The present invention relates to a method (M1) for identifying genes
CC      involved in plant resistance or response to pathogenic infection. M1
CC      comprises identifying a gene whose expression is significantly altered in
CC      the incompatible interaction of plant gene expression relative to
CC      expression of the gene in an uninfected plant, in a mutant plant that
CC      does not express a gene associated with response to pathogenic infection,
CC      or in a corresponding incompatible or compatible interaction. (M1) is
CC      useful for conferring resistance to resistance or tolerance to a plant to
CC      bacterial, fungal or viral infection. The present sequence was used to
CC      illustrate the invention.
XX
SQ      Sequence 1190 BP; 269 A; 330 C; 328 G; 263 T; 0 U; 0 Other;

Query Match      55.4%; Score 822.8; DB 8; Length 1190;
Best Local Similarity 81.2%; Pred. No. 1.2e-228;
Matches 956; Conservative 0; Mismatches 222; Indels 0; Gaps 0;

Qy      80 GAGACATTCCTATTATTCCTCAGAGTCAGTGAACGAGGGGACACCTTGACAGCTCTGCGAC 139
Db      13 GATACCTTCCTCTTTACCTCGGAGTCTGTGAACGAGGGGCCACCTTGACAGCTCTGCGAC 72
Qy      140 CAAATCTCCGATGCTGCTCCGACGCTTGCTTGAACAGGACCCACAGCAAGGTTGCC 199
Db      73 CAAATCTCAGATGCTGTGTTGATGCTGCTGCGCGAGGACCTTGACAGCAAGTGTGCT 132
Qy      200 TCGAAACATGCACCAAGACCAACTTTGGTCTTCGAGAGATCATCCACCAAGGCC 259
Db      133 TGTGAGACCTGCACCAAGACCAACATGGTTCATGGTCTTTGGTGGAGATCATCCACCAAGGCT 192
```

RESULT 5  
ADJ44928  
ID ADJ44928 standard; cDNA; 1191 BP.

```
Qy      260 AACGTTGACTACGAGNAGATCGTGGTGACACCTGCAGGACATCGGCTTGGTCTCAAAC 319
Db      193 AACGTTGACTATGAGAAGATTGTGAGGAGACATCGCGTAACATTCGGTTTTGTGTGAGCT 252
Qy      320 GATGTGGGACTTGATGCTGACAACTGCAAGGTCCTTTGTAACAATTGACGACGAGACCCCT 379
Db      253 GATGTGGGCTTCGATGCTGACCACTGCAAGGTCCTTTGTAACAATTGACGACGAGTCCCT 312
Qy      380 GATATTGCCAGGGTGTGCAAGGCCACTTACCAAAAGACCCGAGGAATAATCGTGTCTGGA 439
Db      313 GACATTGCACAGGGGTGTGACGGGCACCTTACCAGCGCCCTGAGGAGATTGGTGTCTGGT 372
Qy      440 GACAGGGGTACATGTTTGGCTATGCCACGACGAGCAACCCAGAAATTCATGCAATTGAGT 499
Db      373 GACCAGGAGCACATGTTTGGATATGCAACTGATGAGACCCCTGATGATGCCCTCCCTCAGC 432
Qy      500 CATGTTCTTGCAACTAAACTCGGTCTCGTCTCACCGAGGTTTCGCAAGAACGGAACCTGCG 559
Db      433 CATGTCCTTGCTACCAAGCTTGGCGCTGCTTACGGAGGTTTCGCAAGAACGGAACCTGCG 492
Qy      560 CCATGGTTGAGGCTGTGATGGGAAAACCCAAAGTACTGTTGAGTATTACAATGACAAACGGT 619
Db      493 GCATGGCTCAGGCTGTGACGGGAAGACCCCAAGTACTGTTGAGTACCGCAATGAGAGCGGT 552
Qy      620 GCCATGGTTCCAGTTTGGTGTCCCACTGCTCTATCTCCACCAACATGATGAGACTGTG 679
Db      553 GCCAGGTCCTGTCCTGTCCTGTCACACCGCTCTCATCTCTACCCAGCATGATGAGACAGTC 612
Qy      680 ACCAACGACGAAATTCGACGCTGACCTCAAGGAGCATGTGATCAAGCCGGTGTATCCCGAG 739
Db      613 ACCAACGATGAGATTGCTGCTGACTGAAGGAGCATGTGATCAAGCCCTGTCAATCCCGAG 672
Qy      740 AAGTACCTTGATGAGAAGACCAATTTCCACTTGAACCCCTCTGCGCGTTTTGTCTATTGGA 799
Db      673 CAGTACCTTGATGAGAAGACCAATTTCCATCTTAACCCATCTGCTGCTGCTTGTCTATTGGC 732
Qy      800 GGTCTCTACGCTGATGCTGCTCTCACCGCGCGAGATCATCATCGTACTTACCGAGGA 859
Db      733 GGACCTCATGGTGTGCTGGTCTCTACTGCGCGAGAGATCATCATTTGACACTTATGTTGGTGC 792
Qy      860 TGGGCTGCTCATGGTGTGCTGCTTCTCCGGGAAGGATCCCAACCAAGGTTGATAGGAGT 919
Db      793 TGGGAGGCTCACGGTGGTGGTGGCTTCTCTGCGAAGGACCCCAACCAAGGTTGACCGCAGT 852
Qy      920 GGTGCTTACATTTGAGACAGGCTGCTAAGAGCATTTGGCAAGTGGAGTACGACAGAGG 979
Db      853 GGAGCATACGTCGCAAGGCAAGCTGCCAAGAGCATTTGTTGCTAGTGGCTTGTCTGCGCGC 912
Qy      980 TGCATTGTGCAAGTGTCTTATGCCATTGGTGTGCCGAGCCCTTGTCTGTCTTTGTTGAC 1039
Db      913 TGCAATTGTCCAAGTATCATAGCCATCGGTGTCCAGAGCCACTGTCCGTATTCTGTCAC 972
Qy      1040 ACCTATGACACCGGGAAGATCCATGATGAAGAGATTCTCAACATTTGTAAGGAGAACTTT 1099
Db      973 ACATACGGCACTGGCAGGATCCCTGACAAAGAGATCCCTCAAGATTGTGAAGGAGAACTTC 1032
Qy      1100 GATTTACGCGCGGTATGATCTCCATCAACCTTGATCTCAAGAGGGGTGGGATTAACAGG 1159
Db      1033 GACTTCAGGCGCTGGCATGATCATCATCAACCTTGACCTCAAGAAAGCGGCAACGAGCGC 1092
Qy      1160 TTCTTGAAGACTGTCTGATATGGACATTCGCGAGAGAGGACCCCTGACTTTCACATGGGAA 1219
Db      1093 TACCTCAAGAAGCGGCGCTTACGGTCACTTCGGAAGGAGCAGCCCAAGACTTTCACCTGGGAG 1152
Qy      1220 GTGGTCAAGCCCTCAAGTGGGAGAGCCCTAAAGGCCA 1257
Db      1153 GTGGTGAAGCCCTCAAGTGGGAGAGCCCTTCTGCTCA 1190
```

		Matches 953; Conservative 0; Mismatches 225; Indels 0; Gaps 0;	
XX	ADJ44928;		
AC	06-MAY-2004 (first entry)		
DT	Plant cDNA #5928.		
XX			
DE	Plant; gene; ss; transcription; plant genome augmentation; cereal;		
XX	soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet;		
KW	maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance;		
KW	stress tolerance; salt tolerance; cold tolerance; drought tolerance;		
KW	plant nutrition; apical dominance; dwarfism; early flowering; antiviral;		
KW	antifungal.		
XX			
OS	Eukaryota.		
XX			
XX	US2004016025-A1.		
PN			
XX	22-JAN-2004.		
PD			
XX	26-SEP-2002; 2002US-00260238.		
PF			
XX			
PR	26-SEP-2001; 2001US-0325277P.		
PR	26-SEP-2001; 2001US-0325448P.		
PR	04-APR-2002; 2002US-0370620P.		
XX			
PA	(BUDW/) BUDWORTH P.		
PA	(MOUG/) MOUGHAMER T.		
PA	(BRIG/) BRIGGS S P.		
PA	(COOP/) COOPER B.		
PA	(GLAZ/) GLAZEBROOK J.		
PA	(GOFF/) GOFF S A.		
PA	(KATA/) KATAGIRI F.		
PA	(KREP/) KREPS J.		
PA	(PROV/) PROVANT N.		
PA	(RICK/) RICHE D.		
PA	(ZHUT/) ZHU T.		
XX			
PI	Budworth P, Moughamer T, Briggs SP, Cooper B, Glazebrook J;		
PI	Goff SA, Katagiri F, Kreps J, Provant N, Ricke D, Zhu T;		
XX			
XX	WPI; 2004-190374/18.		
DR			
XX			
PT	New rice promoter, useful for manipulating crop plants to alter or		
PT	improve phenotypic characteristics, e.g. produce large quantities of oil		
PT	or proteins, resistance to insecticides, virus or fungi, stress tolerance		
PT	or high nutritional value.		
XX			
PS	Claim 68; SEQ ID NO 5928; 230pp; English.		
XX			
CC	The invention relates to plant nucleotide sequences that direct seed-,		
CC	leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential		
CC	or constitutive transcription of an operatively linked nucleic acid		
CC	segment. The invention also relates to a method for augmenting a plant		
CC	genome and a method of identifying a gene, where its expression is		
CC	altered in the seed, leaf, stem, panicle, pollen, root or is constitutive		
CC	in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower,		
CC	canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,		
CC	sorghum, rice or wheat. The polynucleotides and the polypeptides they		
CC	encode are useful for manipulating crop plants to alter or improve		
CC	phenotypic characteristics, to produce large quantities of oil or		
CC	proteins, to incur resistance to insecticides, viruses or fungi, and to		
CC	incur stress tolerance (e.g. salt, cold or drought) to ensure the plants		
CC	have a high nutritional value with reduced apical dominance or dwarfism,		
CC	early flowering or altered metabolic pathways. This sequence represents a		
CC	plant nucleic acid of the invention. Note: The sequence data for this		
CC	patent did not form part of the printed specification but was obtained in		
CC	electronic format directly from USPTO at <a href="http://seqdata.uspto.gov/sequence.html">seqdata.uspto.gov/sequence.html</a> .		
XX			
SQ	Sequence 1191 BP; 269 A; 329 C; 327 G; 263 T; 0 U; 3 Other;		
XX			
Query Match	55.2%; Score 819.8; DB 12; Length 1191;		
Best Local Similarity	80.9%; Pred. No. 9.2e-228;		

QY 1160 TTCCTGAAGACTGCTGCATATGAGACATTCGGGAGAGAGGCCCTGACTTCATCATGGGAA 1219  
Db 1093 TACCTCAAGACGGCGCTTACGGTCACTTCGGAAGGAGACGACCCAGACTTCACTGGGAG 1152  
QY 1220 GTGGTCAAGCCCTCAAGTGGGAGAGGCTTAAGGCCA 1257  
Db 1153 GTGGTGAAGCCCTCAAGTGGGAGAGGCTTCTGCGCTA 1190

RESULT 6

AAX07183  
ID AAX07183 standard; cDNA; 1582 BP.

XX AAX07183;

21-MAY-1999 (first entry)

XX Corn S-adenosylmethionine synthetase cDNA clone cc3.mn0002.d2.

XX S-adenosylmethionine synthetase; corn; maize; amino acid; lysine;  
KW threonine; methionine; cysteine; isoleucine; transgenic plant;  
KW crop improvement; food; feedstuff; ss.

XX Zea mays.

XX Key Location/Qualifiers  
FH 140.1330  
FT CDS /\*tag= a  
FT  
FT  
XX

PN W09855601-A2.

XX 10-DEC-1998.

XX 05-JUN-1998; 98WO-US011692.

XX 06-JUN-1997; 97US-0048771P.

XX 12-JUN-1997; 97US-0049443P.

XX (DUPO ) DU PONT DE NEMOURS & CO E I.

XX Falco SC, Allen SM, Rafalski JA, Hitz WD, Kinney AJ, Abeil LM;  
PI Thorpe CJ;

XX WPI; 1999-070263/06.

XX P-PSDB; AAW97742.

XX New plant amino acid biosynthetic enzymes, DNA and chimeric genes -  
PT encode: dihydropicolinate reductase; diaminopimelate epimerase; threonine  
PT synthase; threonine deaminase; S-adenosylmethionine synthetase.

XX Claim 41; Page 62-63; 98pp; English.

XX This is the nucleotide sequence of cDNA clone cc3.mn0002.d2, which codes  
CC for a full-length corn S-adenosylmethionine synthetase (see AAW97742).  
CC The clone was isolated from a corn callus cDNA library and identified by  
CC comparison to public sequence databases using BLAST algorithms. It shows  
CC sequence similarity to the *Oryza sativa* enzyme. The invention relates to  
CC new isolated nucleic acid fragments (see AAX07168-85) encoding plant  
CC lysines (see AAW9772-44) that catalyse steps in the biosynthesis of  
CC threonine, methionine, cysteine and isoleucine from aspartate,  
CC the enzyme being selected from dihydropicolinate reductase,  
CC diaminopimelate epimerase, threonine synthase, threonine deaminase or S-  
CC adenosylmethionine synthetase. The invention also relates to the  
CC construction of a chimeric gene encoding all or a portion of the  
CC biosynthetic pathway enzyme, in sense or antisense orientation, where  
CC expression of the chimeric gene results in production of altered levels  
CC of the enzyme in a transformed host cell. Overexpression or reduction of  
CC expression of genes encoding the amino acid biosynthetic pathway enzymes  
CC in crop plants such as corn, soybean and wheat can be used to alter  
CC levels of the amino acids in human food and animal feed. Transformed host  
CC cells can also be used to identify compounds that inhibit one of the  
CC enzymes

XX Sequence 1582 BP; 340 A; 474 C; 417 G; 351 T; 0 U; 0 Other;  
SQ  
Query Match 55.2%; Score 819.6; DB 2; Length 1582;  
Best Local Similarity 81.0%; Pred. NO. 1.2e-227;  
Matches 954; Conservative 0; Mismatches 224; Indels 0; Gaps 0;  
QY 80 GAGACATTCTTATTTACCTCAGAGTCAGTGAACGAGGGACACCTTGACAAGCTCTGCCAC 139  
Db 152 GACACCTTCTCTTCCCTCGGAGTCTGTGAACGAGGGACACCTTGACAAGCTCTGCCAC 211  
QY 140 CAAATCTCCGATGCTCTCGAGCTTGCCTTGAACAGGACCCCAAGAGCAAGGTTCGCC 199  
Db 212 CAGGTCTCAGATGCGCTTCTTGACGCTTGCCTGCTGAGGACCTTGACAGCAAGGTTCGT 271  
QY 200 TCGAACAATGACACCAAGACCAACTTGTCTATGCTTTCGGAGAGATCACCAACCAAGGCC 259  
Db 272 TGTGAGACCTGCACCAAGACCAACATGCTCATGGTCTTTGGTGAATCACCAACCAAGGCC 331  
QY 260 AACGTTGACTAGGAGAGATCGTGGTGACACCTGCAGGACACCTCGGCTTCTCTCAAC 319  
Db 332 AATGTCGACTACGAGAAGATTGTGAGGAGACCTGCGCAACATTTGGTTTGTGTCAAC 391  
QY 320 GATGTGGGACTTGTATGCTGACAACTGCAAGGTCTTTGTAACATTTGACGACGAGCCCT 379  
Db 392 GATGTCGGGCTTGACGCTGACCACTGCAAGGTGCTGCTGAACATTTGACGACGAGTCCCT 451  
QY 380 GATATTGCCAGGGTGTGACGGCCACTTACCAAAAGACCCGAGAGAAATCGTGTCTGGA 439  
Db 452 GATATTGCTCAGGGTGTGATGGCCACTTCAACGAGCGCCCGAGGAGATTGGAGCTGCT 511  
QY 440 GACCAAGGTTCACATGTTTGGCTATGCCAGCGAAGAACCCAGATTCATGCAATTGAGT 499  
Db 512 GACCAGGAGACATGTTTCGGGTATGCGACCCGATGAGACCCCTGAGTTGATGCCCTCAGC 571  
QY 500 CATGTTCTTGCAACTTAAACTCGGTCTCGTCTCACCGAGGTTGCAAGAAACGGAACCTGCG 559  
Db 572 CATGTTCTTGCCACCAAGCTAGGTGCTGCTCTCACCGAGGTCCGCAAGAACGGAACCTGCG 631  
QY 560 CCATGGTTGAGGCTGATGGGAAACCCCAAGTACTGTTGAGTATTACAATGACAAACGGT 619  
Db 632 CCTGGCTCAGGCTGATGGGAAAGCCCAAGGTGACAGTCGAGTACCGCAANTGAGGCTGCT 691  
QY 620 GCCATGGTTCAGTTGGTGTCACACTGCTTATCTCCACCAACATGATGAGACTGTG 679  
Db 692 GCCATGGTTCCTATCCCGTCTCATCTCCACCGACGACGACGACGACGAGTGTG 751  
QY 680 ACCAACGACGAAATTCAGCTGACCTCAAGGAGCATGTGATCAAGCCGGTGTATCCCGGAG 739  
Db 752 ACCAATGATGATGCTGCTGACCTGAAGGAGCATGTGATCAAGCCCTATCATCCCTGAG 811  
QY 740 AAGTACCTTGATGAGAAGACCAATTTTCCACTTGAACCCCTCTGGCGGCTTTGTCTATTGA 799  
Db 812 CAGTACCTTGACGAGAAGACCAATCTTCCACCTTTAACCCATCCGGCGGCTTTGTCTATTGT 871  
QY 800 GGTCTCAGCTGATGCTGGTCTCACCGCCGCAAGATCATCATGATCTTACCGAGGA 859  
Db 872 GGACCTCAGCGGATGCTGGGCTCACTGCGCGCAAGATCATCATTTGACACCTACCGTGGC 931  
QY 860 TGGGGTGTCTATGTTGGTGGTGTCTTCTCCGGGAGGATCCCAACCAAGGTTGATAGGAGT 919  
Db 932 TGGGGAGCCCATGGCGGTGGCGCTTTCTCCGGCAAGGACCCCAACCAAGGTTGACCGCAGC 991  
QY 920 GGTGCTTACATTTGAGACAGCTGCTAAGAGCATTTGGCAAGTGGATAGCCAGAGAG 979  
Db 992 GGAGCCTATGTGCGGAGGACGCTGCCAAGAGCATCTGTCGCGAGCGGCTTTGCTCGCGCG 1051  
QY 980 TGCATTGTGCAAGTCTCTTATGSCCATTTGTCGCCGAGCCCTTCTCTGTCTTTCTTGTGAC 1039  
Db 1052 GCCATGCTCCAGGTGCTCTAGCCATCGCGGTGCCGAGCCCTCTCTCGGTGTTGTGAC 1111  
QY 1040 ACCTATGCGACCGGGAAGATCCATGATAGGAGATTCTCAACATTTGTGAAGGAGAACTTT 1099

Db 1112 ACGTACGGCACCGCGCATCCCGACAAGGAGATCTCAAGATTGTCAGGAGAACTTC 1171  
QY 1100 GATTTCAGGCCCGGTATGATCTCCATCAACCTTGATCTCAAGAGGGGTGGGAATAACAGG 1159  
Db 1172 GATTTCAGGCCCTGGCATGATATCATCACTTGACCTCAAGAAAGCGGCAACGGCGC 1231  
QY 1160 TTCTTGAAGACTGCTGATATGACACTTCGGCAGAGAGACCTGATCTTCAATGGGAA 1219  
Db 1232 TACCTCAAGACGGCAGCTACGGGCCACTTCGGAAGGGACGACCTGACTTCACCTGGGAG 1291  
QY 1220 GTGGTCAAGCCCTCAAGTGGGAGAGCGCCTAAGGCCA 1257  
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## RESULT 7

ADAR70676  
ID ADAR70676 standard; DNA; 1190 BP.

XX AC

ADA70676;

XX 20-NOV-2003 (first entry)

XX Rice gene, SEQ ID 3999.

XX Plant; bacterial infection; fungal infection; viral infection; rice;  
KW gene; ds.

XX Oryza sativa.

XX WO2003000898-A1.

XX 03-JAN-2003.

XX 22-JUN-2001; 2001WO-IB001105.

XX 22-JUN-2001; 2001WO-IB001105.

XX (SYGN ) SYNGENTA PARTICIPATIONS AG.

XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;  
PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;

XX WPI; 2003-175290/17.

XX Identifying at least one gene involved in plant resistance or response to  
PT pathogenic infection for conferring resistance or tolerance to a plant to  
PT bacterial, fungal or viral infection by determining or detecting plant  
PT gene expression.

XX Claim 6; SEQ ID NO 3999; 899pp; English.

XX The present invention relates to a method (M1) for identifying genes  
CC involved in plant resistance or response to pathogenic infection. M1  
CC comprises identifying a gene whose expression is significantly altered in  
CC the incompatible interaction of plant gene expression relative to  
CC expression of the gene in an uninfected plant, in a mutant plant that  
CC does not express a gene associated with response to pathogenic infection,  
CC or in a corresponding incompatible or compatible interaction. (M1) is  
CC useful for conferring resistance to resistance or tolerance to a plant to  
CC bacterial, fungal or viral infection. The present sequence was used to  
CC illustrate the invention.

XX Sequence 1190 BP; 267 A; 335 C; 347 G; 241 T; 0 U; 0 Other;

Query Match 54.8%; Score 813.4; DB 8; Length 1190;

Best Local Similarity 80.8%; Pred. No. 6.7e-226;

Matches 949; Conservative 0; Mismatches 226; Indels 0; Gaps 0;

QY 76 GGCAGAGACATTCCTATTACCTCAGAGTCAGTGAAGGAGGACCCCTGACAGCTCTG 135

Db 9 GGTTGACACCTCTCTTCACTTCCGAGTCCGTCATGAGGGGACACCCCTGACAAAGCTCTG 68

QY 136 CGACCAAAATCTCCGATGCTGTCTCTCGACGCTTTCCTTGAACAGGACCCGACAGCAAGGT 195  
Db 69 CGACCAAGATATCCGATGCGGTGCTTGTATGCGTGCCTTGTGAAGACCCCTGAAGCAAGGT 128  
QY 196 TGCCTCGAAACATGACCAAGACCAACTTGGTTCATGGTCTTTCGGAGAGATCAACACCAA 255  
Db 129 TGCCTGTGAGACTGCAACCAAGACCAACATGGTTCATGGTGTGTTGGTGAGATCACTACCAA 188  
QY 256 GGCCTAACGTTGATCTACGAGAAGATCTGTGCTGACACCTGCAAGAACATCGGCTTCGTCTC 315  
Db 189 GGCCTAATGTTGATCTAGAGAGATCTGTAGGGATATCTTCCCGCGGATCGGCTTGTGTC 248  
QY 316 AAACGATGTGGGACTTGTGATGCTGACAACTGCAAGGTCTTGTGTAACATTTAGAGAGAG 375  
Db 249 CAATGATGTAGGCTTTGATGCTGAACTGTGAAGGTGCTTGTCAAATTTAGAGAGCAATC 308  
QY 376 CCTGATATTTGCCAGGGTGTGCAAGGCCACCTTACCAAAAGACCCGAGGAAATCGGTGC 435  
Db 309 CCTTGACATCGCACAGGGGTGCTCATGGGCACCTTCAACAGCGCCAGAGAGGATTTGGTGC 368  
QY 436 TGGAGACCAAGGTCACATGTTTGGCTATGCCACGACGAAACCCCAAGAAATTTGATGCCATT 495  
Db 369 CGGTGACCAAGGGGATATGTTTGGATATGCAACCGATGAGACCCCTGAAATTTGATGCCACT 428  
QY 496 GAGTCATGTTCTTGGCAACTAAACTCGGTGCTCTCTCACCGAGGTTTCGCAAGAACGGAAC 555  
Db 429 CAGCCATGTTCTTGTCTACCAAGCTCGGTGCGCGTCTCACCGAGGTCGCAAGAACGGGC 488  
QY 556 CTGCCCATGCTTGAAGCCCTGATGGGAAACCCCAAGTGAATTTGATGATTTACATGACAA 615  
Db 489 ATGCGCATGGCTGAGGCTGATGGGAAAGACGCAAGTGACAGTGGAGTACCAAGAACGACAA 548  
QY 616 CGGTGCCATGGTTCCAGTTTCGCTGCCACACTGTGCTTATCTCCACCCCAACATGATGAGAC 675  
Db 549 TGGCGCCATGGTCCCTCTCCGCTCCACACCGTGTCTCATCTCCACCCAGGACGATGAGAC 608  
QY 676 TGTGACCAACGACGAAATTTGACGTGAACCTCAAGGAGCATGTGATCAAGCCGCTGATCCC 735  
Db 609 CGTGACCAACGACGAAATCGCGCTGACCTGAAGGAGCATGTCTCAACCCGTCAGGTCGCTTCAT 668  
QY 736 GAGAGATGACCTTGATGAGAGACCAATTTTCACTTGAACCCCTCTGGCGCGTTTGTCTCAT 795  
Db 669 AGAGCAGTACCTTGTATGAGAAAGCACTTCTTCCATCTCAACCCGTCAGGTCGCTTCAT 728  
QY 796 TGGAGTCTCTCAGGTGATGCTGTCTCACCGCGCAAGATCATCATCGATACTTACCG 855  
Db 729 CGGTGACCTCATGAGATGCAAGTCTCACCGGGCGCAAGATCATCATCGACCTACCG 788  
QY 856 AGGATGGGTGCTCATGTTGTTGCTTTCTCCGGGAAGGATCCCAAGGTTGATAG 915  
Db 789 TGGCTGGGGAGCACACGGTGGTGGCGCTTCTCCGGCAAGGACCCGACCAAGGTTGACCG 848  
QY 916 GAGTGGTGTTCATTTGAGACAGGCTGCTTAAGAGCATTTGGCAAGTGGAGTAGCCAG 975  
Db 849 GAGCGGAGGCTTACATTTGCAAGGAGCGCGGCGCAAGAGCATCGTTGCCAATTTGGCTCG 908  
QY 976 AAGGTGCTTGTGCAAGTGTCTTATGCAATGCTGTGCGCGAGCCCTTCTGTCTTCTTGT 1035  
Db 909 CGCTGCTATTTCCAGGTGTCTATGCCATGCGCTGCGCGAACCGCTCTCGTGTCTGT 968  
QY 1036 TGACACCTATGGCAACCGGGAAGATCATGATAGGAGATTTCTCAACATTTGTGAAGAGAA 1095  
Db 969 CGACACTTACGGCACCGGCAAGATCCCTGACAGGAGATCTCCAGGATTTGTCAAGGAGAA 1028  
QY 1096 CTTTGAATTTAGCGCGGATATGATCTCATCAACCTTGTATCTCAAGAGGGGTGGGATAA 1155  
Db 1029 CTTTGAATTTAGCGCGGAGGATGATCATCAACCTTCAACCTTCAAGAGGGGTGGCAATCG 1088  
QY 1156 CAGGTCTTGTGAAGACTGCTGATATGGAACACTTTCGCGAGAGGACCCCTGACTTACATG 1215  
Db 1089 CCGCTACTGTAAGACGCGGCTTACGCGCATTTCCGGGAGGAGGACCCCTGACTTACCTG 1148  
QY 1216 GGAAGTGGTCAAGCCCTCTCAAGTGGGAGAAAGCGCT 1250



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PR	28-OCT-1999;	99US-0161922P.
PR	28-OCT-1999;	99US-0161933P.
PR	29-OCT-1999;	99US-0162142P.
Query Match 54.2%; Score 804.4; DB 3; Length 1521;		
Best Local Similarity 80.3%; Pred. No. 3.3e-223;		
Matches 943; Conservative 0; Mismatches 231; Indels 0; Gaps 0;		
QY	80	GAGACATTCCTATTTACCTCAGAGTCAAGAGGACACCCCTGACAAAGCTCTGCGAC 139
Db	91	GAATCTTTTGTTCATCTGAATCCGTCAAGAGGACATCCCGACAAAGCTTTGTGAT 150
QY	140	CAATCTCCGATGCTCTCGACGCTTGCCTTGACAGGACCCAGACAGGCTTGC 199
Db	151	CAGATCTCCGACGCTATCTCGATGCTTGCCTTGAACAGACCCCTGAGAGCAAGTTGCT 210

QY	200	TCCGAAACATGCAACCAAGACCACCTTGGTCTATGGTCTTCGGAGAGATCAACCAAGGCC 259
Db	211	TGTGAGACTTGTACCAAGACTAACATGGTCTATGGTCTTGGAGAAATCAACCAAGGCT 270
QY	260	AACGTTGACTAGAGAGATCGTGGTGACACCTCAGGAAACATCGGCTTCGTCTCAAC 319
Db	271	AACGTTGATTACGAGAGATTCTGTAAACATGCCGTGAGATTGGATTCTGTCTCTGCT 330
QY	320	GATGTGGGACTTGTGCTGACAACTGCAAGGTCCTTGTAAACATTTGAGCAGCAGAGCCCT 379
Db	331	GACGTTGGTCTAGATGCTGACAAATTTGCAAGGTTCTGGTTAAACATTTGAGCAACAGAGTCT 390
QY	380	GATATGCCCCAGGGTGTGCAACGGCCACTTACAAAGACCCGAGAGAAATCGGTGCTGGA 439
Db	391	GACATTTGACAAAGGTTTCTGCTCATCTCACAAGAGCCAGAGAGGTTGAGCTGTG 450
QY	440	GACAGGGTCAATGTTGGCTATGCCAGGAGAAACCCAGAAATTTGATGCAATTTGAT 499
Db	451	GACCAAGGTCAATGTTGGGTATGCTACTGATGAGACTCTCTGAGCTCATGCTCTTACT 510
QY	500	CATGTTCTTGCAACTAAACTCGGTGCTCTCTCACCGAGGTTTCGCAAGAACGGAACTTCG 559
Db	511	CACGTTCTCGTACTTAAGCTTGGAGCTAAACTCACTGAAGTTTCGCAAGAAATGGAATTCG 570
QY	560	CCATGGTTGAGGCTGATGGGAAACCCCAAGTGACTGTTGAGTATTTCAATGACAAACGGT 619
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QY	620	GCCATGGTTCCAGTTGCTGTCACACTGTGCTTATCTCCACCCACATGATGAGACTG 679
Db	631	GCCATGGTTCCTGTAGCTGCACACTGTTCTCATCTCAACACAGCATGACGAGACTGTG 690
QY	680	ACCAACGACGAAATTCGACGCTGACCTCAAGAGAGATGTGATCAAGCCGGTGTATCCCGAG 739
Db	691	ACTAACGATGATGCGAGCTGATCTTAAGGAGCATGTGATCAAGCCAGTGTATCCAGAG 750
QY	740	AAGTACCTTGATGAGAACCAATTTTCCATTGAAACCCCTCTGGCCGTTTTGTCTATGGA 799
Db	751	AAATACCTTGATGAGAAACCAATCTTCCATCTCAACCCATCTGCTGCTTTGTTATCGGA 810
QY	800	GSTCCTCAGGTTGATGCTGCTCAACGGCCGACAGATCATCATGATATTTACGGAGA 859
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Db	871	TGGGGTGACACGAGGTTGGTCTTCTCTGGAAGGAGCCCAACCAAGGTTGACAGAGT 930
QY	920	GGTGTCTTACATTTGTGAGACAGGCTCTAAGAGCATTTGGCAAGTGGACTAGCCAGAGG 979
Db	931	GGGGCTTACATCGTTAGGCAAGCAGCTAAGAGCATTTGTAGCCAGTGGGCTAGCGAGCGG 990
QY	980	TGCATTTGTCAAGTGTCTTATGCCATTGGTGGCCGAGCCCTTTGCTCTCTTTGTTGAC 1039
Db	991	GTCATTTGTCAAGTCTCGTATGCCATTGGTGTCTTCTGAGCCATTGTGTGTCTGTTGGAC 1050
QY	1040	ACCTATGCAACGGGAAGATCATCATTAAGGAGATTCTCAACATTTGTGAAGGAGAACTTT 1099
Db	1051	AGTTATGGAACAGGAAGATACCAAGCAAGGAGATTTCTTGAGATTTGTGAAGGAGATTTT 1110
QY	1100	GATTTGAGGCGCGGTATGATCTCCATCAACCTTGTATCTCAAGAGGGGTGGGAATACAGG 1159
Db	1111	GATTTGAGGCGCGGTATGATCTCCATTAACCTTGGATCTGAGAGAGGAGGTAATGGTAGG 1170
QY	1160	TTCTTGAAGACTGCTGCATATGGACACTTCGGCAGAGAGGACCTTGACTTCACTGAGNA 1219
Db	1171	TTCTTGAAGACTGCTGCCTATGGTCACTTTTGAAGGAGCAGTGTGATTTTCACTCTGGAG 1230
QY	1220	GTGTCAGGCGCTCAAGTGGGAGAGGCTTAAG 1253
Db	1231	GTAGTCAAGCCACTCAAGTCTTAACGAGGTCGAG 1264



RESULT 9  
AAC33986  
ID AAC33986 standard; DNA; 1508 BP.  
XX  
AC AAC33986;  
XX  
DT 17-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 5035.  
XX  
KW Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway; metabolic pathway;  
KW promoter; termination sequence; ss.  
XX  
XX Arabidopsis thaliana.  
OS  
PN BP1033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2008EP-00301439.  
XX  
PR 25-FEB-1999; 99US-0121825P.  
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PR 12-AUG-1999; 99US-0148341P.  
PR 13-AUG-1999; 99US-0148565P.  
PR 13-AUG-1999; 99US-0148684P.  
PR 16-AUG-1999; 99US-0149368P.  
PR 17-AUG-1999; 99US-0149175P.  
PR 18-AUG-1999; 99US-0149426P.  
PR 20-AUG-1999; 99US-0149722P.  
PR 20-AUG-1999; 99US-0149723P.

PR	20-AUG-1999;	99US-0149929P.
PR	23-AUG-1999;	99US-0149902P.
PR	23-AUG-1999;	99US-0149930P.
PR	25-AUG-1999;	99US-0150566P.
PR	26-AUG-1999;	99US-0150884P.
PR	27-AUG-1999;	99US-0151065P.
PR	27-AUG-1999;	99US-0151066P.
PR	27-AUG-1999;	99US-0151080P.
PR	30-AUG-1999;	99US-0151303P.
PR	31-AUG-1999;	99US-0151438P.
PR	01-SEP-1999;	99US-0151930P.
PR	07-SEP-1999;	99US-0152363P.
PR	10-SEP-1999;	99US-0153070P.
PR	13-SEP-1999;	99US-0153758P.
PR	15-SEP-1999;	99US-0154018P.
PR	16-SEP-1999;	99US-0154039P.
PR	20-SEP-1999;	99US-0154779P.
PR	22-SEP-1999;	99US-0155139P.
PR	23-SEP-1999;	99US-0155486P.
PR	24-SEP-1999;	99US-0155659P.
PR	28-SEP-1999;	99US-0156458P.
PR	29-SEP-1999;	99US-0156596P.
PR	04-OCT-1999;	99US-0157117P.
PR	05-OCT-1999;	99US-0157753P.
PR	06-OCT-1999;	99US-0157865P.
PR	07-OCT-1999;	99US-0158029P.
PR	08-OCT-1999;	99US-0158232P.
PR	12-OCT-1999;	99US-0158369P.
PR	13-OCT-1999;	99US-0159293P.
PR	13-OCT-1999;	99US-0159294P.
PR	13-OCT-1999;	99US-0159295P.
PR	14-OCT-1999;	99US-0159329P.
PR	14-OCT-1999;	99US-0159330P.
PR	14-OCT-1999;	99US-0159331P.
PR	14-OCT-1999;	99US-0159637P.
PR	14-OCT-1999;	99US-0159638P.
PR	18-OCT-1999;	99US-0159584P.
PR	21-OCT-1999;	99US-0160741P.
PR	21-OCT-1999;	99US-0160767P.
PR	21-OCT-1999;	99US-0160768P.
PR	21-OCT-1999;	99US-0160770P.
PR	21-OCT-1999;	99US-0160814P.
PR	21-OCT-1999;	99US-0160815P.
PR	22-OCT-1999;	99US-0160980P.
PR	22-OCT-1999;	99US-0160981P.
PR	22-OCT-1999;	99US-0160989P.
PR	25-OCT-1999;	99US-0161404P.
PR	25-OCT-1999;	99US-0161405P.
PR	25-OCT-1999;	99US-0161406P.
PR	26-OCT-1999;	99US-0161359P.
PR	26-OCT-1999;	99US-0161360P.
PR	26-OCT-1999;	99US-0161361P.
PR	28-OCT-1999;	99US-0161920P.
PR	28-OCT-1999;	99US-0161992P.
PR	28-OCT-1999;	99US-0161993P.
PR	29-OCT-1999;	99US-0162142P.
Query Match 54.1%; Score 802.8; DB 3; Length 1508;		
Best Local Similarity 80.2%; Pred. No. 9.5e-223;		
Matches 942; Conservative 0; Mismatchces 232; Indels 0; Gaps 0;		
QY	80	GAGACATTCCTATTTACCTCAGAGTCAGTGAACGAGGGGACACCCCTGACAAAGCTCTGCGAC 139
DB	93	GAATCTTTTGTTCACATCTGAATCCGTCAACGAGGGGACATCCGACAAAGCTTTGTGAT 152
QY	140	CAAAATCCGATGCTGCTCCTGACGGCTTGCCTTTGAACAGGACCCAGACAGCAAGGTTGCC 199
DB	153	CAGATCCGACGCTATCTCCTGATGCTTGCCTTTGAACAGACCCCTGAGAGCAAAAGTTGCT 212
QY	200	TCGGAACATGCACCAAGACCAACTTGGTCATGGTCTTCGGAGAGATCACCAACCAAGGCC 259
DB	213	TGTGAGACTTGTACCAAGACTAAACATGGTCTATGGTTTTTGGAGAAATCACCAACCAAGGCT 272

RESULT 10  
ADA67853  
ID ADA67853 standard; DNA; 1182 BP.  
XX

QY	260	AACGTTGACTACGAGAAGATCGTGCGTGACACCTGCGAGAAACATCGCGCTTCGTCCTCAAAC 319
DB	273	AACGTTGATTACGAGCAGATTTGTCGTAATAACATGCGCGTGAATTCGATTCGATCTGCT 332
QY	320	GATGTGGGACTTGATGCTGACAACTGCAAGGTCCTTGTAAACATTCAGCAGCAGAGCCCT 379
DB	333	GACGTTGGTCTAGATGCTGACAAATTCGAAGGTTCTGGTTAAACATTCAGCAACAGAGTCCT 392
QY	380	GATATTGCCCCAGGCTGTCACGCGCCACCTTTACCAAAAGACCCGAGGAAATCGGTGCTGGA 439
DB	393	GACATTGCAACAAGGTTTCATGGTCATCTCACCAAGAACCCAGAGAGGTTGGAGTGGT 452
QY	440	GACCAAGGTCACATGTTTGGCTATGCCACGACGAAACCCAGAAATTCGATTCGATTCGAT 499
DB	453	GACCAAGGTCACATGTTTGGGTCATGCTACTGATGAGACTCTCTGAGCTCATGCTCTTACT 512
QY	500	CATGTTCTTGCAACTTAACTCGGTGCTCTCACCGAGGTTCCGCAAGAACCGAACCTGC 559
DB	513	CACGTTCTCGCTACTAAGCTTCGAGCTAACTCACTGAAGTTTCGCAAGAAATGGAACCTGC 572
QY	560	CCATGGTTGAGGCTGATGGGAAACCCAAAGTGAATGTTGAGTATTTCAATGACAAACGGT 619
DB	573	CCTTGGTTGAGGCCAGATGGTAAGACTCAAGTCACTATTGAGTACATCAACGAAACGGA 632
QY	620	GCCATGGTTCCAGTTGCTGTCACACTGTGCTTATCTCCACCAACATGATGAGACTGTG 679
DB	633	GCCATGGTTCTGTACTGTCACACTGTTCTCATCTCAACACAGCATCAGCAGACTGTG 692
QY	680	ACCAACGACGAAATTCGACGCTGACCTCAAGGAGCATGTGNTCAAGCCGCTGATCCCGGAG 739
DB	693	ACTAAGCATGAGATCGCAGCTGATCTTAAGGAGCATGTGATCAAGCCAGTGTATCCAGAG 752
QY	740	AAGTACCTTGATGAGAAGACCAATTTCCACTTGAACCCCTCTGGCGGTTTTGTCATTGGA 799
DB	753	AAATACCTTGATGAGAAGAACCAATCTTCCATCTCAACCCATCTGTTGCTTTGTTGATCGGA 812
QY	800	GGTCTCTCAGGTCATGCTGCTCACCAGCCGCAAGATCATCATCGATATTCATCGAGAGA 859
DB	813	GGTCTCTCAGGATGTCAGGGCTTACCGGCGCTAAGATCATCATCGATATTCATCGAGAGT 872
QY	860	TGGGGTCTCATGGTGGTGGTCTTCTCCGGGAAGATCCCAACAGGTTGATAGGAGT 919
DB	873	TGGGGTGCACACGAGGTTGGTCTTCTCTGGAAGGACCCCAACAGGTTGACAGGAGT 932
QY	920	GGTCTCTACATTTGTCAGACAGCTCTAAGAGCATTTGTGGCAAGTGGACTAGCCAGAGG 979
DB	933	GGGGCTTACATCGTTAGGCAAGCAGCTAAGAGCATTTGACGAGTGGGCTAGCAGGCGG 992
QY	980	TGCATTGTGCAAGTGTCTTATGCCATTCGTTGCCGAGCCCTTCTGCTGTTTGTGAC 1039
DB	993	GTCAATTGTGCAAGTCTCGTATGCCATTGGTGTCTCCCTGAGCCATTCTCTGTGTTCTGGAC 1052
QY	1040	ACCTATGSCACCGGGAAGATCCATGATTAAGAGATTTCTCAACATTTGTGAGAGAGACTTT 1099
DB	1053	AGTTATGGAACAGGAAAGATACCAGAACAGGAGATTTCTTGAGATTTGTGAAGGAGAGTTT 1112
QY	1100	GATTTCCAGCCCGGTATCATCTTCCATCAACCTTGATCTCAAGAGGGTGGGAATAACAGG 1159
DB	1113	GATTTCCAGCCAGGATGATGATCTCCATTAACCTTGGATCTGAAGAGAGGAGGTTAATGGTAG 1172
QY	1160	TTCTTGAAGACTGCTGCATATGGACATTTCCGACAGAGAGCCCTGACTTCAATGAGGAA 1219
DB	1173	TTCTTGAAGACTGCTGCCTATGGTCACITTTGGAAGGAGCATGCTGATTTTCACTCTGGAG 1232
QY	1220	GTGTCAGGCCCTCAAGTGGGAGAGGCCCTAAG 1253
DB	1233	GTAGTCAAGCCACTCAAGTCTAAACAGGTCCAAG 1266





PR	20-SEP-1999;	99US-0154779P.
PR	22-SEP-1999;	99US-0155139P.
PR	23-SEP-1999;	99US-0155486P.
PR	24-SEP-1999;	99US-0155659P.
PR	28-SEP-1999;	99US-0156458P.
PR	29-SEP-1999;	99US-0156596P.
PR	04-OCT-1999;	99US-0157117P.
PR	05-OCT-1999;	99US-0157753P.
PR	06-OCT-1999;	99US-0157865P.
PR	07-OCT-1999;	99US-0158029P.
PR	08-OCT-1999;	99US-0158232P.
PR	12-OCT-1999;	99US-0158369P.
PR	13-OCT-1999;	99US-0159293P.
PR	13-OCT-1999;	99US-0159294P.
PR	13-OCT-1999;	99US-0159295P.
PR	14-OCT-1999;	99US-0159329P.
PR	14-OCT-1999;	99US-0159330P.
PR	14-OCT-1999;	99US-0159331P.
PR	14-OCT-1999;	99US-0159637P.
PR	14-OCT-1999;	99US-0159638P.
PR	18-OCT-1999;	99US-0159584P.
PR	21-OCT-1999;	99US-0160741P.
PR	21-OCT-1999;	99US-0160767P.
PR	21-OCT-1999;	99US-0160768P.
PR	21-OCT-1999;	99US-0160770P.
PR	21-OCT-1999;	99US-0160814P.
PR	21-OCT-1999;	99US-0160815P.
PR	22-OCT-1999;	99US-0160980P.
PR	22-OCT-1999;	99US-0160981P.
PR	22-OCT-1999;	99US-0160989P.
PR	25-OCT-1999;	99US-0161404P.
PR	25-OCT-1999;	99US-0161405P.
PR	25-OCT-1999;	99US-0161406P.
PR	26-OCT-1999;	99US-0161359P.
PR	26-OCT-1999;	99US-0161360P.
PR	26-OCT-1999;	99US-0161361P.
PR	28-OCT-1999;	99US-0161920P.
PR	28-OCT-1999;	99US-0161922P.
PR	28-OCT-1999;	99US-0161993P.
PR	29-OCT-1999;	99US-0162142P.

Query Match 53.6%; Score 796.4; DB 3; Length 1393;

Best Local Similarity 79.9%; Pred. No. 6.7e-221;

Matches 938; Conservative 0; Mismatches 236; Indels 0; Gaps 0;

QY	80	GAGACATTCCTATTACCTCAGAGTCAAGTGAACGAGGGACACCCCTGACAAAGCTCTGCGAC	139
DB	98	GAGACTTTCCTATTACATCTGAGTCTGTGAACGAAGGACACCCCTGACAAAGCTTTGCGAC	157
QY	140	CAAACTCCGATGCTGTCTCGAGCTTCGAGCTTGCCTTGAACGAGCCGACAGCAAGGTTGCC	199
DB	158	CAGATCTCTGATGCACTCTTGTATGCTGCTTGAAGAACCCCTGATAGCAAGTTGCT	217
QY	200	TGCGAAACATGACCAAGACCAACTTGGTCTTCGAGAGATCACCAAGGCTC	259
DB	218	TGTGACATATGACCAAGACCAACATGGTCTATGGTTTCGGTGAGATCACCAAGGCT	277
QY	260	AACGTTTACTACGAGAAGATCGTGTGACACCTGCGAGAAACATCGGCTTCGCTCAAC	319
DB	278	ACGATTGACTACGAGAAGATTTGCCGTGACACTTGGCGTTCCATTGGATTCTCTGAC	337
QY	320	GATGTGGGACTTGACTGACAACTGCAAGTCTTGTAAACATTTGAGCAGCAGGCCCT	379
DB	338	GATGTGGTCTTGATGCTGACAAATGCAAAAGTCTTGTGTAAACATTTGACCAAGGCCA	397
QY	380	GATATTGCCAGGGTGTGACCGCCACCTTACCAAAAGACCCGAGGAAATCGGTGTGGA	439
DB	398	GACATTGCTCAAGGTGTTTACGGTCACTTACCAAAAGTCCAGAGACATTTGAGCTGT	457
QY	440	GACCAAGGTCATATGTTTGGCTATGCCAGGAGAAACCCCAAGATTTGATGCAATGAGT	499
DB	458	GACCAAGGACACATGTTTGGTTATGCCATGTGATGAACCCCTGAGCTCATGCTCTTGAGT	517

QY	500	CATGTTCTTGCAACTAAACTCGTGCTCGTCTCACCGAGGTTGCAAGAACGAACTGC	559
DB	518	CATGCTCTTGCAACCAAGATTGGTGCTCGTCTCACTGAAGTCAGGAAGATGGAACTGC	577
QY	560	CCATGGTTGAGCCCTGATGGGAAAAACCAAGTACTGTTGAGTATTACAATGACAAAGGT	619
DB	578	CGTTGGTTAAGACCAAGATGGCAAGACCACAGTCACTGTTGAGTACTACATGACAAATGC	637
QY	620	GCCATGGTTCAGTTCGTTCCACACTGTGCTTATCTCCACCCCAACATGATGAGACTGTG	679
DB	638	GCTATGGTTCAGTCCGTTCTCACACCGTCTGATCTCAACCCAGCAGATGAAACCGTT	697
QY	680	ACCAACGACGAAATTCAGCTGACCTCAAGAGACATGTGATCAAGCCCGTGTATCCCGAG	739
DB	698	ACCAATGACGAGATTGCGCGTGACCTCAAGAGACATGTGATCNAACCAATCATCCAGAG	757
QY	740	AAGTACCTTGATGAGAAGACCATTTTCCATTGAAACCCCTCTGGCCGTTTTGTTCATGGA	799
DB	758	AAATACCTTGACGACAAAACCATCTTCCACCTCAACCCCATCAGGCCGTTTGTGATCGGG	817
QY	800	GGTCTCTCAGGCTGATGCTGGTCTCACCGGCCGACAGATCATCATCTTACCGAGA	859
DB	818	GGACCAACGCGTGATGCTGGTTTAACTCGACGTAAAGATCATCATTTGACACATACCGAGA	877
QY	860	TGGGTGCTCATGGTGGTGTCTTCTCCGGGAAGGATCCCAAGGTTGATAGGAGT	919
DB	878	TGGGAGCTCATGGAGTGGTGTCTTCTCAGGCAAGACCCCAACCAAGTCGACAGAGT	937
QY	920	GGTGCTTACATTTGTGAGACAGGCTGTAAAGACATTTGTGGCAAGTGGACTAGCCAGAGG	979
DB	938	GGAGCTTACATCGTGGAGCAAGAGAGTGTGGTGGCTTAATGGCATGGCTCGCAGG	997
QY	980	TGCATTGTCAAGTGTCTTATGCCATTGGTGTGCCGAGCCCTTGTCTGTCTTGTTCAC	1039
DB	998	GCTCTTGTCCAGGCTCTCATACGCCATTGGAGTACCCGAGCCATTGTCTGTCTTGTTCAC	1057
QY	1040	ACCTATGGCACCGGGAAGATCATGATAAGGAGATTCTCAACATTTGTAAGGAGAACTTT	1099
DB	1058	ACTTACGGAAACAGGTTGATTTCCAGACAAAGAGATCCTGAGATCTGTGAAGAGACATTC	1117
QY	1100	GATTTACGCCCCGGTATGATCTCCATCAACCTTGTATCTCAAGAGGGGTGGGAATAACAGG	1159
DB	1118	GATTTACAGACCAGGAATGATGACAATCACTTGGACTTGAAGAGAGGAGGAAATGGAAGG	1177
QY	1160	TTCTTGAAGACTGTGCAATATGGACATTCGGCAGAGAGGACCCCTGACTTTCACATGGGA	1219
DB	1178	TTTCAGAAAACGGCAGCGTATGGACATTTTCGGAAGAGACGACCCCTGACTTTCACCTGGGAG	1237
QY	1220	GTGGTCAAGCCCTCAAGTGGGAGAAAGCCCTAAG	1253
DB	1238	GTCGTGAAGCCACTCAAGTGGGACAAACCTCAAG	1271

RESULT 12

AAT99141

ID AAT99141 standard; cDNA to mRNA; 1182 BP.

XX AAT99141;

AC AAT99141;

DT 26-MAR-1998 (first entry)

XX S-adenosylmethionine synthase 1 gene.

XX S-adenosylmethionine synthase 1 gene; barley; alkali resistant plant; sami; ss.

XX Hordeum vulgare.

XX JP09313186-A.

XX 09-DEC-1997.

XX 28-MAY-1996; 96JP-00133406.



CC does not express a gene associated with response to pathogenic infection,  
CC or in a corresponding incompatible or compatible interaction. (M1) is  
CC useful for conferring resistance to resistance or tolerance to a plant to  
CC bacterial, fungal or viral infection. The present sequence was used to  
CC illustrate the invention.

XX Sequence 1185 BP; 235 A; 440 C; 346 G; 164 T; 0 U; 0 Other;

Query Match 53.0%; Score 786.4; DB 8; Length 1185;  
Best Local Similarity 79.7%; Pred. No. 5e-218;  
Matches 941; Conservative 0; Mismatches 236; Indels 3; Gaps 1;

QY 71 AGATGGGACAGACATTCCTATTACTCAGAGTCACTGAGGAGGACACCTCCAGCAAG 130  
DB 1 ATGGCGGGAGACGTTCTCTTCACCTCCGAGTCCGTGAACGAGGTCACCCCGACAG 60  
QY 131 CTCTGCGACCAATCTCCGATGTCTCTCGACGCTTTCCTTTGAACAGACCCAGACAGC 190  
DB 61 CTGTGCGACCAAGTGTGCGACGGGTCTCGACGGTCTCGCCAGGACCCCGACAGC 120  
QY 191 AGGTTGCTGCGAACAATGACCAAGACCACTTGTGTCATGGTCTTCGGAGAGATCACC 250  
DB 121 AAGTGGCGTGGCAGACGTCACCAAGACCAACATGGTGTATGGTTCGGCGAGATCACC 180  
QY 251 ACCAAGGCCAAGTGTGACCTACGAGAGATCGTGGTGACACCTGCGAGAACATCGGCTTC 310  
DB 181 ACCAAGGCCAAGTGTGACCTACGAGAGATCGTGGTGACACCTGCGCGACACCTCGCGGATCGGCTTC 240  
QY 311 GTCTCAAAAGTGTGGGACTTGTATGTGACAACTGCAAGGTCTTGTAAACATTTGAGCAG 370  
DB 241 GTGTCCGACGAGTGGCTCGACCGCGACCGCTGCAAGGTCTCGTCAACATCGAGCAG 300  
QY 371 CAGAGCCCTGATTTATGCCAGGGTGTGACGGGACCTTACCAAGACCCGAGGAATC 430  
DB 301 CAGTCCCGGACATCGCGAGGGGTGCAAGGACCTTCCAAAGCGCCCGAGGAGATC 360  
QY 431 GGTGTGAGAGACAGGTCACATGTTTGTGCTATGCGACGAGCAACCCCAATTTGATG 490  
DB 361 GGGCGGGCGACAGGGCCACATGTTGCGGTACGCCACCGACGAGACCCCGAGCTGATG 420  
QY 491 CCAATTGAGTCATGTTCTTGCAATAAATCGGTGCTGCTTCAACGAGGTTCGCAAGAAC 550  
DB 421 CCCTCAGCAGCATCTCTCCACCAAGCTCGGCGCGCTCACCAGGTTCGCAAGAAC 480  
QY 551 GGAACCTGCCATGTTGAGGCTGATGGGAAACCCAGTACTGTTGAGTATTACAT 610  
DB 481 GGCACCTGGCGCTGCTGAGGCGGACCGGACAGCCAGGTCAACGTTGAGTACCTCAAC 540  
QY 611 GACACGGTGCCATGTTCCAGTTCAGTTCACACTGTGCTTATCTCCACCCCAACATGAT 670  
DB 541 GACCGCGGCGCATGTTCCCGTCCGCTCCACCGTCTCATCTCCACCCGACGAC 600  
QY 671 GAGACTGTGACCAACGACGAAATTTGAGTGCACCTCAAGGAGCATGTGATCAAGCGGTG 730  
DB 601 GAGACGTCACCAACGACGAGATCGCGCGACCTCAAGGAGCATGTGATCAAGCGGTG 660  
QY 731 ATCCCGGAGAGTACCTTGTGAGAGACATTTTCCACTTGAACCCCTCTGCGCGTTT 790  
DB 661 ATCCCGGACAGTACCTGACGAGAGACATTTTCCACTTGAACCCCTCTGCGCGTTT 720  
QY 791 GTCAATGGAGGTCTCTCAGCGTGTGCTGCTCAGCGCGGCAAGATCATCATCATCT 850  
DB 721 GTCAATGGGCGGCGGCGGCGGCGGCGGCTTCCAGCGGCGGAGNATCATCATCGACAC 780  
QY 851 TAGCGAGGATGGGGTCTCATGTTGTTGTTGTTCTCCGGAAGGATCCCAAGGTT 910  
DB 781 TAGCGGAGATGGGCGGCGGCGGCGGCGGCTTCTCCGGAAGGATCCCAAGGTT 840  
QY 911 GATAGAGTGGTCTTACATTTGTGACACAGGCTGCTTAAGAGCATTTGCAAGTGCATTA 970  
DB 841 GACCGGAGGCGGCTTACATTCGCGAGGCGGCGGCGGCGGATGTCGCCAGCGGCTTC 900  
QY 971 GCCAAGAGTGTGTCAGAGTGTCTTATGCAATGTTGTTGTCGCCGAGCGCTTGTCTGTC 1030

DB 901 GCCCGCGCTGCATCGTGCAGGTCTGTACGCCATCGCGTCCCGAGCCGCTCTCCGTCG 960  
QY 1031 TTGTTGACACTTATGGCACCGGGAAGATCATGATAGGAGATTTCTCAACATTTGTGAAG 1090  
DB 961 TTGTTGACTCTTACGGCACCGGCAAGATCCCGCAAGGAGATCTCAAGATCGTCAAG 1020  
QY 1091 GAGAACTTGTATTCAGCGCGGTATGATCTTCCATCACTTGTATCTCAAGAGGGTGGG 1150  
DB 1021 GAGAACTTGTATTCAGCGCGGTATGATGATCACTCAACCTCGACCTCAAGAGGGCGG- 1079  
QY 1151 AATAACAGGTTCTTGAAGACTGCTGCATATGACACATTTCCGCGAGAGAGACCTGACTTC 1210  
DB 1080 --CAACCGGTTTCATCAAGACCGCGGCGTACCGCATTTCCGCGGAGGATCCCGACTTC 1137  
QY 1211 ACATGGGAGTGTGTCAGCCCTCAAGTGGGAGAGGCTT 1250  
DB 1138 ACATGGGAGTGTGTCAGCCCTCAAGTGTGAGAGGCT 1177  
RESULT 14  
AAC33674  
ID AAC33674 standard; DNA; 1395 BP.  
XX AC AAC33674;  
XX AC AAC33674;  
DT 17-OCT-2000 (first entry)  
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 3906.  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 3906.  
KW Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway; metabolic pathway;  
KW promoter; termination sequence; ss.  
XX Arabidopsis thaliana.  
XX EP1033405-A2.  
PD 06-SEP-2000.  
XX 25-FEB-2000; 2000EP-00301439.  
XX 25-FEB-1999; 99US-0121825P.  
PR 05-MAR-1999; 99US-0123180P.  
PR 09-MAR-1999; 99US-0123548P.  
PR 23-MAR-1999; 99US-0125788P.  
PR 25-MAR-1999; 99US-0126264P.  
PR 29-MAR-1999; 99US-0126785P.  
PR 01-APR-1999; 99US-0127462P.  
PR 06-APR-1999; 99US-0128234P.  
PR 08-APR-1999; 99US-0128714P.  
PR 16-APR-1999; 99US-0129845P.  
PR 19-APR-1999; 99US-0130077P.  
PR 21-APR-1999; 99US-0130449P.  
PR 23-APR-1999; 99US-0130510P.  
PR 23-APR-1999; 99US-0130891P.  
PR 28-APR-1999; 99US-0131449P.  
PR 30-APR-1999; 99US-0132048P.  
PR 30-APR-1999; 99US-0132407P.  
PR 04-MAY-1999; 99US-0132484P.  
PR 05-MAY-1999; 99US-0132485P.  
PR 06-MAY-1999; 99US-0132486P.  
PR 06-MAY-1999; 99US-0132487P.  
PR 07-MAY-1999; 99US-0132863P.  
PR 11-MAY-1999; 99US-0134258P.  
PR 14-MAY-1999; 99US-0134218P.  
PR 14-MAY-1999; 99US-0134219P.  
PR 14-MAY-1999; 99US-0134221P.  
PR 14-MAY-1999; 99US-0134370P.  
PR 18-MAY-1999; 99US-0134768P.  
PR 19-MAY-1999; 99US-0134941P.  
PR 20-MAY-1999; 99US-0135124P.  
PR 21-MAY-1999; 99US-0135353P.



PR 24-MAY-1999; 99US-0135629P.  
PR 25-MAY-1999; 99US-0136021P.  
PR 27-MAY-1999; 99US-0136392P.  
PR 28-MAY-1999; 99US-0136782P.  
PR 01-JUN-1999; 99US-0137222P.  
PR 03-JUN-1999; 99US-0137528P.  
PR 04-JUN-1999; 99US-0137502P.  
PR 07-JUN-1999; 99US-0137724P.  
PR 08-JUN-1999; 99US-0138094P.  
PR 10-JUN-1999; 99US-0138540P.  
PR 10-JUN-1999; 99US-0138847P.  
PR 14-JUN-1999; 99US-0139119P.  
PR 16-JUN-1999; 99US-0139452P.  
PR 17-JUN-1999; 99US-0139453P.  
PR 17-JUN-1999; 99US-0139492P.  
PR 18-JUN-1999; 99US-0139454P.  
PR 18-JUN-1999; 99US-0139455P.  
PR 18-JUN-1999; 99US-0139456P.  
PR 18-JUN-1999; 99US-0139457P.  
PR 18-JUN-1999; 99US-0139458P.  
PR 18-JUN-1999; 99US-0139459P.  
PR 18-JUN-1999; 99US-0139460P.  
PR 18-JUN-1999; 99US-0139461P.  
PR 18-JUN-1999; 99US-0139462P.  
PR 18-JUN-1999; 99US-0139463P.  
PR 18-JUN-1999; 99US-0139750P.  
PR 18-JUN-1999; 99US-0139763P.  
PR 21-JUN-1999; 99US-0139817P.  
PR 22-JUN-1999; 99US-0139899P.  
PR 23-JUN-1999; 99US-0140353P.  
PR 23-JUN-1999; 99US-0140354P.  
PR 24-JUN-1999; 99US-0140695P.  
PR 28-JUN-1999; 99US-0140823P.  
PR 29-JUN-1999; 99US-0140991P.  
PR 30-JUN-1999; 99US-0141287P.  
PR 01-JUL-1999; 99US-0141842P.  
PR 01-JUL-1999; 99US-0142154P.  
PR 02-JUL-1999; 99US-0142055P.  
PR 06-JUL-1999; 99US-0142390P.  
PR 08-JUL-1999; 99US-0142803P.  
PR 09-JUL-1999; 99US-0142920P.  
PR 12-JUL-1999; 99US-0142777P.  
PR 13-JUL-1999; 99US-0143542P.  
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PR 29-OCT-1999; 99US-0162142P.  
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XX AC AAT99143;  
XX DT 26-MAR-1998 (first entry)  
XX DE S-adenosylmethionine synthase 3 gene.  
XX KW S-adenosylmethionine synthase 3 gene; barley; alkali resistant plant;  
XX OS sam3; ss.  
XX PN Hordeum vulgare.  
XX PD JP09313186-A.  
XX PF 09-DEC-1997.  
XX PR 28-MAY-1996; 96JP-00133406.  
XX PA (NIOC ) NIPPON OIL CO LTD.  
XX DR WPI; 1998-080077/08.  
XX P-PSDB; AAW34542.  
XX PT S-adenosyl-methionine synthase gene - useful in producing plants  
XX PT resistant to alkaline soil.  
XX PS Claim 6; Page 10-11; 13pp; Japanese.  
XX CC This sequence represents the S-adenosylmethionine synthase 3 (sam3) gene.  
XX CC This DNA sequence may be used in a vector to produce plants which are  
XX CC resistant to alkaline soil  
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Query Match 52.4%; Score 778.6; DB 2; Length 1182;  
Best Local Similarity 79.2%; Pred. No. 9.3e-216;  
Matches 938; Conservative 0; Mismatches 244; Indels 3; Gaps 1;  
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Search completed: August 31, 2005, 01:31:36  
Job time : 819.183 secs

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2	866.8	58.4	1479	4	US-09-424-978B-40	Sequence 40, Appl
3	821.4	55.3	2193	4	US-09-424-978B-37	Sequence 37, Appl
4	819.6	55.2	1582	4	US-09-424-978B-35	Sequence 35, Appl
5	777.8	53.1	1353	4	US-09-424-978B-43	Sequence 43, Appl
6	787.8	52.4	1380	4	US-09-424-978B-41	Sequence 41, Appl
7	422.4	28.4	1283	3	US-09-949-016-4188	Sequence 4188, Ap
8	420.8	28.3	1283	3	US-09-318-448-22	Sequence 22, Appl
9	420.8	28.3	1283	4	US-09-023-655-1371	Sequence 1371, Ap
10	420.8	28.3	3435	4	US-09-976-594-470	Sequence 470, App
11	411.4	27.7	3220	4	US-09-949-016-1787	Sequence 1787, Ap
12	411.4	27.7	3228	3	US-09-318-448-20	Sequence 20, Appl
13	411.4	27.7	3228	4	US-09-949-016-68	Sequence 68, Appl
14	384.8	25.9	1173	4	US-09-248-796A-4152	Sequence 4152, Ap
15	306.8	20.7	1158	4	US-09-489-039A-4746	Sequence 4746, Ap
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17	303.8	20.5	1470	4	US-09-252-991A-3329	Sequence 3239, Ap
18	291.6	19.6	1208	2	US-08-403-852D-4	Sequence 4, Appli
19	291.6	19.6	1208	3	US-08-510-646B-4	Sequence 4, Appli
20	291.6	19.6	1208	3	US-09-231-818-4	Sequence 4, Appli
21	291.6	19.6	1208	4	US-09-635-359B-4	Sequence 4, Appli
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26	289.2	19.5	1164	4	US-09-543-681A-2958	Sequence 2958, Ap
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RESULT 2  
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; Sequence 40, Application US/09424978B  
; Patent No. 6664445  
; GENERAL INFORMATION:  
; APPLICANT: Falco, Saverio Carl  
; APPLICANT: Allen, Stephen M.  
; APPLICANT: Rafalski, J. Antoni  
; APPLICANT: Hitz, William D.  
; APPLICANT: Kinney, Anthony J.  
; APPLICANT: Abell, Lynne N.  
; APPLICANT: Thorpe, Catherine J.  
; TITLE OF INVENTION: Plant Amino Acid Biosynthetic Enzymes  
; FILE REFERENCE: BB-1087  
; CURRENT APPLICATION NUMBER: US/09/424,978B  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: US 60/048,771  
; PRIOR FILING DATE: 1997-06-06  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 40  
; LENGTH: 1479  
; TYPE: DNA  
; ORGANISM: Lycopodium obscurum  
US-09-424-978B-40  
  
Query Match 58.4%; Score 866.8; DB 4; Length 1479;  
Best Local Similarity 81.5%; Pred. No. 5.7e-259;  
Matches 1003; Conservative 0; Mismatches 227; Indels 0; Gaps 0;  
  
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Db 403 ACATTGAGCAGCAAAAGTCTGATATTTGCTCAAGGTGTCCACCGCCATCTGACCAACGCC 462  
QY 420 CCGAGGAATCGGTCTCGAGACCAAGGCTCACATGCTTTGGCTTATGCCCGAGCAACCC 479  
Db 463 CCGAGGAATTTGGTCTGGTACCAGGGCCACATGTTTGGCTTATGCCAGATGAGACCC 522  
QY 480 CAGAAATTCATTCATTTGATGATGTTCTTGTCAAACTGCAAACTCGTCTCAGCCAGG 539  
Db 523 CTGAATTAATGCTCTCAGTCAAGTCTTGAACCTTGAACCTTGTGCTGCTTACAGAG 582  
QY 540 TTTCCAGAAACGGAACCTTGCCCATGGTTGAGGCTGATGGGAAACCCCAAGTGTGTTG 599  
Db 583 TCCGCAAGAAATGGCACTTGGCTGCTGCTGAGGCTGATGGCAAGACCCCAAGTTACTGTTG 642

600 AGTATTACATGACACGGTGCATGTTCCAGTTCGTGTCACACATGTCCTTATCTCCA 659  
643 AGTATAGCAATGACAAATGGTGCATGTTCCAAATAGGGTACACACTGTTCTTATCTCCA 702  
660 CCCAACATGATGAGACTGTGACCAACGACGAAATTCAGCTGACCTCAAGGACATGTGA 719  
703 CCCAACAGATGAGACCGTTACCAATGATGAGATGCCCCGACCTTAAAGGACATGTGA 762  
720 TCAAGCCGGTGTATCCCGGAGAGTACCTTGATGAGAGACCAATTTTCCACTTGAAACCCCT 779  
763 TCAACACAGTATCCCGAGAGATACCTTGATGAGAACTACTATTTTCCACCTTAAACCAT 822  
780 CTGGCCGTTTGTATTTGAGAGTCTCAGCGTATGCTGCTCTCAACCGGCGGCAAGATCA 839  
823 CTGGCCGATTCGTTATTTGGTGGACCTCATGGTATGCTGCTCTCACTGGTCTGTAATAATCA 882  
840 TCATCATATCTTACGGAGAGATGGGTGCTCATGGTGGTGGTCTTCTCCGGGAAGATC 899  
883 TCATCGACACTTATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 942  
900 CCACCAAGTGTGATAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 959  
943 CAACCAAGTTCGACAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1002  
960 CAAGTGGACTAGCCAGAGGTGCATTTGTGCAAGTGTCTTATGCAATTTGGTGTGCCCGAGC 1019  
1003 CTAGTGGACTGCTGCTAGATGATCGTGCAGGTATCTTATGCCATCGGTGGTGGTGGTGGTGG 1062  
1020 CTTTGTCTGTTTGTGACACCTATGGCACCGGGAAGATCCATGATAGAGAGATCTCA 1079  
1063 CATTTGTCTGTTTGTGACACCTATGGCACCTGGAAGATCCCTGACAGGAAATTTTGA 1122  
1080 ACATTGTGAAGGAGAACTTTGATTTCCAGCCGGTATGATCTCCATCAACCTTTGATCTCA 1139  
1123 AGATGTTAAGGAGAACTTTGATTTCCAGCTGGAAATGATGTCATTAATCTTGGATTTGA 1182  
1140 AGAGGGGTGGGAATACAGGTTCTTGAAGACTGCTGATATGACACTTCCGACAGAGG 1199  
1183 AGAGGGGTGGCAATAGAACTTTGAAACTGCTGCTATGTCATTTGGACGTGATG 1242  
1200 ACCCTGACTTCATCGGGAAGTGGTCAAGCCCTCAAGTGGGAGAGGCTTAAGGCCATT 1259  
1243 ACCCCGATTTCAATGGGAAGTTGTCAAGCCCTCAAGTGGGAAAGGCCCAAGACTAAT 1302  
1260 CATTCCTGCAATGCTGGGAGTTTTTT 1289  
1303 AAGTCTTCCCTATGTTTGTCTTTGTT 1332

## RESULT 3

US-09-424-978B-37  
; Sequence 37, Application US/09424978B  
; Patent No. 6664445  
; GENERAL INFORMATION:  
; APPLICANT: Falco, Saverio Carl  
; APPLICANT: Allen, Stephen M.  
; APPLICANT: Rafalski, J. Antoni  
; APPLICANT: Hitz, William D.  
; APPLICANT: Kinney, Anthony J.  
; APPLICANT: Abell, Lynne N.  
; APPLICANT: Thorpe, Catherine J.  
; TITLE OF INVENTION: Plant Amino Acid Biosynthetic Enzymes  
; FILE REFERENCE: BB-1087  
; CURRENT APPLICATION NUMBER: US/09/424,978B  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: US 60/048,771  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 37  
; LENGTH: 2183  
; TYPE: DNA

ORGANISM: Oryza sativa  
US-09-424-978B-37

Query Match 55.3%; Score 821.4; DB 4; Length 2183;  
Best Local Similarity 80.6%; Pred. No. 1e-244;  
Matches 960; Conservative 0; Mismatches 231; Indels 0; Gaps 0;  
QY 80 GAGACATTCCTATTTACCTCAGAGTCAGTGAACAGGGGACACCTGTGACAAAGCTCTGCGAC 139  
DB 800 GATACCTCTCTCTTTACCTCGGAGTCTGTGAACGAGGGCCACCTGTGACAAAGCTCTGCGAC 859  
QY 140 CAAATCTCCGATGCTCTCGACCTTGCCTTGAACAGGAGCCACAGACGAGGTGGC 199  
DB 860 CAAATCTCAGATGCTCTCGACCTTGCCTTGAACAGGAGCCCTGTGACAAAGGTGCGT 919  
QY 200 TCGGAAAACATGCAACCAAGACCAATTTGGTCAATGGTCTTCGAGAGATACACCAAGGCGC 259  
DB 920 TGTGAGACTGCAACCAAGACCAATTTGGTCAATGGTCTTCGAGAGATACACCAAGGCGT 979  
QY 260 AACGTTGACTACGAGAAAGATCGTGTGACACCTCGAGAAACATCGGCTTCGTCTCAAAAC 319  
DB 980 AACGTTGACTACGAGAAAGATCGTGTGACACCTCGAGAGATACACCAAGGCGT 1039  
QY 320 GATGTGGACTTGTGCTGACAACTGCAAGGTCTTGTAAACATTTGAGCAGCAGAGCCCT 379  
DB 1040 GATGTGGTCTGATGCTGACCACTGCAAGGTCTTGTAAACATCGAGCAGCAGTCCCT 1099  
QY 380 GATATTGCCAGGGTGTGCAAGCCACCTTACCAAAAGACCCGAGAAATCGGTGCTGGA 439  
DB 1100 GATATTGCCAGGGTGTGCAAGCCACCTTACCAAGCCCTTGAAGAGATTTGGTGTGCT 1159  
QY 440 GACCAAGGCTCAATGTTTGGCTATGCCAGGACGAAACCCAGAAATTTGATGCCATTTGAGT 499  
DB 1160 GACCAAGGACACATGTTTGGATATGCAACTGATGAGACCCCTGAGTGTGATGCCCCCTCAGC 1219  
QY 500 CATGTTCTTGCACATTAACCTGCTGCTCTCAACGAGGTTCGCAAGAACCGAAACCTGTC 559  
DB 1220 CATGTCCTTGTACCAAGCTTGGCGCTGCTCTTACGAGGTTTCGCAAGAACCGAAACCTGTC 1279  
QY 560 CCATGTTGAGGCTGTGAGGAAACCAAGTGTGCTGATGATGATGATGATGATGATGATGATGAT 619  
DB 1280 GCATGGCTCAGGCTGTGAGGAAACCAAGTGTGCTGATGATGATGATGATGATGATGATGATG 1339  
QY 620 GCATGGTTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 679  
DB 1340 GCCAGGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1399  
QY 680 ACCAACGACAAATTCAGCTGACCTCAAGGAGCATGTGATCAAGCCCGGTGATCCCGGAG 739  
DB 1400 ACCAACGATGAGATTTGCTGCTGACCTGAAGGAGCATGTGATCAAGCCCTGCTCAATCCCGAG 1459  
QY 740 AAGTACCTTGTGAGAGACCAATTTTCCATTTGAACCCCTTGGCCGCTTGTGCTCATTTGA 799  
DB 1460 CAGTACCTTGTGAGAGACCAATTTTCCATTTGAACCCCTTGGCTGCTGCTGCTGCTGCTGCT 1519  
QY 800 GGTCTCTCAGGTGATGCTGCTGCTCAACCGGCGCAAGATCATCATCGATCTTACCGAGGA 859  
DB 1520 GGACCTCATGTTGATGCTGCTGCTCACTGCGCGGAGAGATCATCATTTGACATTTATGCTGGC 1579  
QY 860 TGGGGTGTCTCATGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 919  
DB 1580 TGGGGAGCTCAGGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1639  
QY 920 GGTGCTTACATTTGAGACAGCTGCTGAAGCATTTGCGCAAGGATCCCAACCAAGGTGATAGGAGT 979  
DB 1640 GGAGCATACGTCGCAAGGCAAGCTGCTGAAGGAGCATTTGTTGCTAGTGGGCTTGTGCTCGCCGC 1699  
QY 980 TGCATTGTGCAAGTGTCTTATGCCATTTGGTGGCCGAGCCCTTGTGCTGCTGCTGCTGCTGCTG 1039  
DB 1700 TGCATTGTGCAAGTGTCTTATGCCATTTGATGCCATTTGATGCCATTTGATGCCATTTGATGCC 1759  
QY 1040 ACCTATGGCACCGGAGAGATCCATGATTAAGGAGATTTCTCAACATTTGTGAAGGAGAACTTT 1099



Db 1760 ACATACGGCACTGGCAGGATCCTGACAGGAGATCTCTCAAGATTGTGAAGGAGAACTTC 1819  
Qy 1100 GATTTCAGCCCGGTATGATCTCCATCAACCTTGATCTCAAGAGGGTGGGATACAGG 1159  
Db 1820 GACTTCAGGCGTGGATGATCATCATCAACCTTGATCTCAAGAAAGGGCGCAACGGAGCG 1879  
Qy 1160 TTCTTGAAGACTGCTGATATGACACTTTCGGCAGAGAGACCTTGACTTTCACATGGGAA 1219  
Db 1880 TACCTCAAGACGGCGCTTACCGTCACTTCGGAAGGAGCAGCCAGACTTTCACCTGGGAG 1939  
Qy 1220 GTGGTCAAGCCCTCAAGTGGGAGAGGCTTAAGGCCATTCAATCCACTGC 1270  
Db 1940 GTGGTGAAGCCCTCAAGTGGGAGAGGCTTCTGCTAAAGCTCCCTTTC 1990

## RESULT 4

US-09-424-978B-35  
; Sequence 35, Application US/09424978B

; Patent No. 6664445

; GENERAL INFORMATION:

; APPLICANT: Falco, Saverio Carl

; APPLICANT: Allen, Stephen M.

; APPLICANT: Rafalski, J. Antoni

; APPLICANT: Hitz, William D.

; APPLICANT: Kinney, Anthony J.

; APPLICANT: Abell, Lynne N.

; APPLICANT: Thorpe, Catherine J.

; TITLE OF INVENTION: Plant Amino Acid Biosynthetic Enzymes

; FILE REFERENCE: BB-1087

; CURRENT APPLICATION NUMBER: US/09/424,978B

; CURRENT FILING DATE: 1999-12-02

; PRIOR APPLICATION NUMBER: US 60/048,771

; PRIOR FILING DATE: 1997-06-06

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 35

; LENGTH: 1582

; TYPE: DNA

; ORGANISM: Zea mays

US-09-424-978B-35

Query Match 55.2%; Score 819.6; DB 4; Length 1582;

Best Local Similarity 81.0%; Pred. No. 3e-244;

Matches 954; Conservative 0; Mismatches 224; Indels 0; Gaps 0;

Qy 80 GAGACATTCTATTACCTAGAGTCAGTGAACGAGGGACACCCCTGACAAAGCTCTGGAC 139  
Db 152 GACACCTTCTCTTCACTCGGAGTCTGTGAACGAGGGACACCCCTGACAAAGCTCTGGAC 211  
Qy 140 CAATCTCCGATGCTGTCTCGACGCTTGCCTTGAACGAGCCCGACAGCAAGGTTGCC 199  
Db 212 CAGGTCAGATGCGCGTCTTGACGCTTGCCCTTGCTGAGGACCCCTGACAGCAAGGTTGCT 271

Qy 200 TGGAAACATGCACCAAGACCACTTGGTCTTCGGAGAGATCAACCAAGGCC 259  
Db 272 TGTGAGACCTGCACCAAGACCAACATGTCATGCTTTTGGTGAGATCAACCAAGGCC 331  
Qy 260 AACGTTGACTACGAGAAGATCGTGCCTGACACCTGCAGGAAACATCGGCTTCGCTCAAAC 319  
Db 332 AATGTCGACTACGAGAAGATTGTGAGGAGACCTCGCGCAACATTTGGTTTGTGTCAAAC 391  
Qy 320 GATGTGGGACTTATGCTGACACTGCAAGTCTTGTAAACANTTGACGAGCAGGACCT 379  
Db 392 GATGTGCGGCTTGACGCTGACCACTGCAAGGTTGCTCGTGAACATTTGAGCAGAGTCCCT 451

Qy 380 GATATTGCCAGGGTGTGCAGCGCCACCTTACCAAAAGACCCGAGGAATCGGTGCTGGA 439  
Db 452 GATATTGCTCAGGGTGTGCATGGCCACTTCACCAAGCGCCCGGAGAGATTGAGCTGCT 511  
Qy 440 GACCAGGGTCAATGTTTGGCTATGCCAGGACGAAACCCCAAGATTGATGCCATTGAT 499  
Db 512 GACCAGGGAACATGTTTCGGGTATGCCAGCGATGAGACCCCTGAGTTGATGCCCTCAGC 571

Qy 500 CATGTTCTTGCAACTAACTCGGTCTGCTCTCACGAGGTTTCGCAAGAACGGAACTCTGC 559  
Db 572 CATGTCCTTGCCACCAAGCTAGGTGCTCGTCTACCGAGGTCCGCAAGAACGGAACTCTGC 631  
Qy 560 CCATGGTTGAGGCTGATGGGAAACCCCAAGTGAATGTTGAGTATTACAATGACAAACGGT 619  
Db 632 CCCTGGCTCAGGCTGATGGGAAGACCCAGGTGACAGTCGAGTACCGCAATGAGGGTGGT 691  
Qy 620 GCCATGGTTCCAGTTCGTTGTCACACTGTCTTATCCACCCCAACATGATGAGACTGTG 679  
Db 692 GCCATGGTCCCACATCCCGTGTCCACACCGTCTCATCTCCACCCAGCAGACGACAGTGT 751  
Qy 680 ACCAACGACGAAATTCAGACTGACCTCAAGGAGCATGTGATCAAGCCGGTGTATCCCGAG 739  
Db 752 ACCAATGATGATCGCTGCTGACCTGAAGGAGCATGTGATCAAGCCCTATCATCCCTGAG 811  
Qy 740 AAGTACCTTGATGAGAGAACCATTTTCCATTGAAACCCCTCTGGCCGTTTGTCTATTGGA 799  
Db 812 CAGTACCTTGACGAGAAAGACCATCTTCCACCTTAACCCATCCGCGCTTTGTCTATTGGT 871  
Qy 800 GGTCTCAGCGTGATGCTGTCTCACCGCGCGCAAGATCATCATCGACTTTACCGAGGA 859  
Db 872 GGACCTCAGCGGATGCTGGGCTCACTGGCCGCAAGATCATCATTTGACACCTACGGTGGC 931  
Qy 860 TGGGCTGCTCATGGTGGTGGTCTTCTCCGGGAAGGATCCCAAGGTTGATAGGAGT 919  
Db 932 TGGGAGGCCATGGCGTGGCGCTTCTCCGGCAAGGAGCCCAACCAAGGTTGACCGCAGC 991  
Qy 920 GGTGCTTACATTGTGAGACAGGCTGTAAAGCATTTGTGGCAAGTGGACTAGCCAGAAAG 979  
Db 992 GGAGCTATGTCCGGAGCGAGGCTGCCAAGAGCATCGTCCGCGAGCGGCTTGTCTCGCGC 1051  
Qy 980 TGCATTGTGCAAGTGTCTTATGCCATTGTGTCGCCAGGCTTGTCTGTCTTGTGTGAC 1039  
Db 1052 GCCATGTCCTCAGGTTCTCTAGCCATCGCGCTGCCCGAGCCCTCTCTCGTGTGTGAC 1111  
Qy 1040 ACCTATGACCGGGAAGATCATGATAAGGAGATTCTCAACATTGTGAAGGAGAACTTT 1099  
Db 1112 ACGTACGGCACGGCGCATCCCCGCAAGGAGATCCTCAAGATTGTCAAGGAGAACTTC 1171  
Qy 1100 GATTTCAGGCGCGGTATGATCTCCATCAACCTTGTATCTCAAGAGGGTGGGATTAACAGG 1159  
Db 1172 GATTTCAGGCTTGGCATGATTATCATCAACCTTGACCTCAAGAAAGGGCGCAACGGGCGC 1231  
Qy 1160 TTCTTGAAGACTGCTGCATATGGACACTTCGCGAGAGGACCTGACTTTCATCATGGGAA 1219  
Db 1232 TACCTCAAGACGGAGCGCTACGGCCACTTCGGAAGGAGCAGCCCTGACTTTCACCTGGGAG 1291  
Qy 1220 GTGGTCAAGCCCTCAAGTGGGAGAGGCGCTAAGGCCA 1257  
Db 1292 GTGGTGAAGCCACTCAAGTGGGAGAAACCTTCTGCGCTA 1329

## RESULT 5

US-09-424-978B-43

; Sequence 43, Application US/09424978B

; Patent No. 6664445

; GENERAL INFORMATION:

; APPLICANT: Falco, Saverio Carl

; APPLICANT: Allen, Stephen M.

; APPLICANT: Rafalski, J. Antoni

; APPLICANT: Hitz, William D.

; APPLICANT: Kinney, Anthony J.

; APPLICANT: Abell, Lynne N.

; APPLICANT: Thorpe, Catherine J.

; TITLE OF INVENTION: Plant Amino Acid Biosynthetic Enzymes

; FILE REFERENCE: BB-1087

; CURRENT APPLICATION NUMBER: US/09/424,978B

; CURRENT FILING DATE: 1999-12-02

; PRIOR APPLICATION NUMBER: US 60/048,771

; PRIOR FILING DATE: 1997-06-06

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn version 3.1

```
; SEQ ID NO 43
; LENGTH: 1353
; TYPE: DNA
; ORGANISM: Hordeum vulgare
US-09-424-978B-43

Query Match      53.1%; Score 787.8; DB 4; Length 1353;
Best Local Similarity 77.8%; Pred. No. 2.2e-234;
Matches 964; Conservative 0; Mismatches 272; Indels 3; Gaps 1;

QY  71  AAGATGCGCAGACATTCCTATTACCTCAGAGTCAAGTGAACGAGGACACCTCGACAAG 130
DB  55  ATGCGCGCGAGAGCTTCCTCTTACGTCGAGTCCGTGAACGAGGCGCATCCGACAAG 114
QY  131  CTCTGCGACCAATCTCGATGCTCTCTCGACGCTTGCCCTGAACAGGACCCGACAGC 190
DB  115  CTGTGCGACCAAGTCTCTGACGCGCTCTTGACGCGCTCTTGCGCCGAGGATCCTGACAGC 174
QY  191  AAGGTTGCGTGGCAACATGCAACAGACCAACTTGGTCATGCTCTCGAGAGATCACC 250
DB  175  AAGGTTGCTTGGCAGACCTGSCACCAAGACCAACATGGTCATGGTCTTTCGCGGAGATCACC 234
QY  251  ACCAAGCGCAACCTTGACTACGAGAAGATCGTGCCTGACACCTGCGAGAACATCGGCTTC 310
DB  235  ACCAAGCGCAACCTTGACTATGAGAAGATTGTGCGGACACCTGCGTGACATCGGCTTC 294
QY  311  GTCTCAAAAGANTGGGACTTGATGCTGACAACTGCAAGTCTCTGTAAACATTTGAGCAG 370
DB  295  ATCTCTGAGACGCTGCTCGATGCGGACCACTTGCAAGGTGCTCGTCAACATCGAGCAG 354
QY  371  CAGAGCCCTGATATTGCGCAGGCTGTGACGCGCACCTTACCAAAAGACCCGAGGAAATC 430
DB  355  CAAATCCCTGACATTTGCCAGGCTGTTCACGGACACTTCAACAAAGGCTCGAGAAGAGGTC 414
QY  431  GGTGCTGGAGACAGAGTCAATGTTGGTGTGCTATGCGACGACGAAACCCAGAAATGATG 490
DB  415  GCGCGCGGTGACAGGCGCATCATGTTTGGCTACGCCACTGATGAGACCCCTGAGCTGATG 474
QY  491  CCATTGAGTCATGTTCTTGCAACTAAACTCGGTGCTCGTCTCAACCGAGGTTTCGCAAGAAC 550
DB  475  CCCTCACCACATGCTTGCCACCAAGCTCGGAGCTCGCTCAACCGAGTCCGCAAGAT 534
QY  551  GGAACCTGCCATGTTGAGGCTGATGGGAAACCCCAAGTGAATCTGTTGAGTATTAAT 610
DB  535  GGCACCTGCGCTGCTGAGGCTGATGGAAAGACCCAGCTCAACATGAGTACCTAAAC 594
QY  611  GACAAAGGTCGCAATGTTCCAGTTCGTGTCACACTGCTTATCTCCACCCCAACATGAT 670
DB  595  GAGGTTGTCGCAATGTTGCGGCTGCTGTCGTCACACCTCTCTATCTCCACCCAGCATGAT 654
QY  671  GAGACTGTGACCAACGCAAAATTCAGCTGACCTCAAGGAGCATGTGATCAAGCCGGTG 730
DB  655  GAGACGTCACCAACCATGAGATCGTGCAGACCTCAAGGAGCATGTATCAAGCCGGTG 714
QY  731  ATCCCGGAGAAGTACCTTGATGAGAAGACATTTTCCATTGAAACCCCTCTGCGCGTTT 790
DB  715  ATTCCCGGAAGTACCTCGATGAGAACACCATCTTCCACTGAAACCATCGGCGCGCTTT 774
QY  791  GTCATTTGAGGTCCTCAACGATGATGCTGCTCAACGCGCGCAAGATCATATCGATCT 850
DB  775  GTCATCGTGGCCCTCACGCGATGCGGCTCTCACGCGCGCAAGATCATATCGACACC 834
QY  851  TAGCGAGGATGGGCTGCTCATGTTGTTGTTGCTTTCTCGGGAAGGATCCCAACAGGTT 910
DB  835  TATGTTGGTGGGAGCCCAACGCGCGGTGCTTCTTGGCAGAGACCCCTACCAAGGTC 894
QY  911  GATAGAGTGGTCTTACATTTGAGACAGGCTGCTTAAGACCATTTGCGCAAGTGA 970
DB  895  GACCGCAGTGGCGCTTACATTTGCGAGGCTGCGCAAGAGCATCATCGCAGCGGCTC 954
QY  971  GCCAGAGTGCATTTGCAAGTCTTATGCAATGTTGTTGCGCGAGCTTTGCTGTC 1030
DB  955  GCAACGCGGTGCAATTTGTCAGATCTCATATGCAATCGGTTGATACCTGAGCGCTTTGTCGTG 1014
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; SEQ ID NO 41
; LENGTH: 1380
; TYPE: DNA
; ORGANISM: Triticum aestiva
US-09-424-978B-41

Query Match      52.4%; Score 777.8; DB 4; Length 1380;
Best Local Similarity 79.0%; Pred. No. 2.9e-231;
Matches 933; Conservative 4; Mismatches 241; Indels 3; Gaps 1;

QY  77  GCAGAGACATTCCTATTTACCTCAGAGTCAGTGAACGAGGACCCCTGACAGCTCTGC 136
DB  79  GCGGAGAGCTTCCTCTTACGTCGAGTCTGTGAACGAGGCGCATCCGACAGCTCTGT 138
QY  137  GACCAAAATCTCGAGTGTCTCTCGACGCTTGCCTTGAAACAGGACCCGACAGCAAGGTT 196
DB  139  GACCAAGTCTCGACGCGCTCTGTGATGCTGCTTGGCCAGGATGCGGACAGCAAGGTC 198
QY  197  GCCTCGGAAAATGACCAAGACCAACTTTGGTTCATGTTCTTCGGAGAGATCAACCAAG 256
DB  199  GCCTCGGAGACCGCTCAACAGACCAACATGGTTCATGGTCTTGGGCGAGATCAACCAAG 258
QY  257  GCCAAGTGTGATGATGCTGACAACTGCAAGGTCCTTGTAAACATTCGGCTTCGTCCTCA 316
DB  259  GCCAAGTGTGATGATGCTGACAACTGCAAGGTCCTTGTAAACATTCGGCTTCGTCCTCA 318
QY  317  AACGATGTGGGACTTGTGATGCTGACAACTGCAAGGTCCTTGTAAACATTCGGCTTCGTCCTCA 376
DB  319  GATGAGTGTGCTCGACGCGCATCGTGTGAAGTGTGCTGCTCAACATTCGAGCAGCAGTCC 378
QY  377  CCTGATATTGCCAGGCTGTGACGCGCCACCTTTACCAAAAGACCCGAGGAAATCGGTGCT 436
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RESULT 6  
US-09-424-978B-41  
; Sequence 41, Application US/09424978B  
; Patent No. 6664445  
; GENERAL INFORMATION:  
; APPLICANT: Falco, Saverio Carl  
; APPLICANT: Allen, Stephen M.  
; APPLICANT: Rafalski, J. Antoni  
; APPLICANT: Hitz, William D.  
; APPLICANT: Kinney, Anthony J.  
; APPLICANT: Abell, Lynne N.  
; APPLICANT: Thorpe, Catherine J.  
; TITLE OF INVENTION: Plant Amino Acid Biosynthetic Enzymes  
; FILE REFERENCE: BB-1087  
; CURRENT APPLICATION NUMBER: US/09/424,978B  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: US 60/048,771  
; FILING DATE: 1997-06-06  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 41  
; LENGTH: 1380  
; TYPE: DNA  
; ORGANISM: Triticum aestiva  
US-09-424-978B-41





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/ FILING DATE: HEREWITH
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Zeller, Karen J.
/ REGISTRATION NUMBER: 37,071
/ REFERENCE/DOCKET NUMBER: PA-0001 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (650) 855-0555
/ TELEFAX: (650) 845-4166
/ INFORMATION FOR SEQ ID NO: 1371:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1283 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: GENBANK
/ CLONE: G36326
/ US-09-023-655-1371

Query Match      28.3%; Score 420.8; DB 4; Length 1283;
Best Local Similarity 62.4%; Pred. No. 4.4e-120;
Matches 700; Conservative 0; Mismatches 407; Indels 15; Gaps 2;

QY 76 GGAGAGACATTCCTATTACCTCAGAGTCAGTGAAAGGAGACACCTCGACAAGCTCTG 135
D 107 GGAGGGCACATTCCTTTTCACTCAGAGTCGGTGGGGAAGGCCACCCAGATAAAGATTG 166

QY 136 CGACCAAACTCCGATGCTCTCGACCTTGCCTTGAACAGGACCCAGACAGCAAGT 195
D 167 TGACCAAAATCAGTGATGCTTCTTGATGCCACCTTCAGCAGGATCTCGAATGCCAAA 226

QY 196 TGCTCGCAAAATGATGACCAAGACCAACTTGTGTCATGCTTTCGGAGAGATCACCACAA 255
D 227 AGCTTGTGAACCTGTGTAAACTGGAATGATCTTCTTGTGGGGAATTCATCTCAG 286

QY 256 GGCAACAGTTGACTACGAGAAAGATCGTGTGACACCTGACAGAAATCGGCTTCGTC 315
D 287 AGCTGTGTGACTACGAGAAAGTGTGCTGAAGCTGTGAACACATTTGGATATGATGA 346

QY 316 AAACAGATGGGACTGTGATGCTGACAACTGCAAGTCTTGTAAACATTTGACACAG 375
D 347 TTCTTCAAAGGTTTGTACTCAAGACTTTGTAACGTGCTGTGTAGCTTTGGAGCAAC 406

QY 376 CCTGATATTGCCAGGGTGTGCACGGCCACCTTACCAAAAGACCCGAGGAATCGGTGC 435
D 407 ACCAGATATTGCTCAAGTGT-----TCATCTTGACAGAAATGAAGAGACATTTGGTGC 460

QY 436 TGGAGACAGGTTCACATTTTGGCTATGCCACGAGCAAAACCCAGAAATTTGATCCCAT 495
D 461 TGGAGACAGGGCTTAATTTTGGCTATGCCACTGATGAACTGAGGAGTGTATGCCCTT 520

QY 496 GAGTCATGTTCTTGCACTAAACTCGGTGCTCTCACCGAGGTTCCGACAGAAAGCAAC 555
D 521 AACCATTTGCTTGGCACACAACTAAATGCCAAACTGCGAGAACTACCGCGTAATGGCAC 580

QY 556 CTGCCCATGTTGAGCGCTGATGGGAAACCCCAAGTACTGTGTAGTATTACAATGACAA 615
D 581 TTTGCTTGTGTTACGCGCTGATTTCTAAAACTCAAGTTACTGTGAGTATATGACAGATCG 640

QY 616 CGGTGCAATGGTTCACATTTGTTGTCACACTGTGCTTATCTCCACCCCAACATGATGAGAC 675
D 641 AGGTGCTGTGCTTCCCATCAGAGTCCACAAATTTGTTATCTGTTTCAGCATGATGAAGA 700

QY 676 TGTGACCAACAGCAAAATTTGAGCTGACCTCAAGAGCATGTGATCAAGCCGCTGATCCC 735
D 701 GGTTTGTCTGTGATGAAATGAGGGATGCCCCCTAAAGGAGAAAGTCATCAAGACGATTTG 760

QY 736 GGAGAAAGTACCTTGTATGAGAAGACCAATTTTCCACTTTGAACCCCTCTGGCCGTTTGT 795
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Db 761 TGCGAATACCTTGTATGAGGATACAAATCTACCACTACAGCAAGTGGCAGATTGTTAT 820
QY 796 TGGAGGTCTCTACCGTGATGCTGTGCTCACCGGCGCAAGATCATCATCTTACCTTAC 855
D 821 TGGTGGGCTCAGGGTGATGCTGTGTTTGACTGAGCGGAAATCATTTGTGGACATTTAT 880
QY 856 AGGATGGGGTCTCATGTTGGTGTGCTTCTCCGGAAGGATCCCAAGGTTGATAG 915
D 881 CGTTTGGGTGCTCATGAGAGGAGTGCCTTTTTCAGGAAAGATTTATCAAGGTCGACCG 940
QY 916 GAGTGTGCTTTACATTTGTGACACAGGCTGTCTAAGAGCATTTGTGGCAAGTGGAC 975
D 941 TTCAGCTGCTTATGCTGCTCGTTGGTGGCAAAATCCCTTCTTAAAGAGGCTCTGTGCG 1000
QY 976 AAGTGTGATTTGTGCAAGTGTCTTATGCAATTTGGTGTGCGCCGAGCTTTGTCTGTT 1035
D 1001 GAGGTTCTTGTTCAGGTCCTTATGCTATTTGGAGTTTCTCATCAATTTATCTCTCCAT 1060
QY 1036 TGACACCTATGCGACCGGAGATCCATGATAAGAGATTTCTCAACATTTGTGAAGGAAA 1095
D 1061 TTTCAATTTATGTTACCTCTCAGAAAGATGAGAGAGCTATTAGAGATTGTGAAGAGAA 1120
QY 1096 CTTTGAATTTAGGCCCCGCTATGATCTCCATCAACCTTGTATCTCAAGAGGGTGGGAATA 1155
D 1121 TTTGATCTCCGCTCGGCTCATTTGTCAGGATCTCGATCTGAAGAAGCCCAATTTATCA 1180
QY 1156 CAGGTTCTTGAAGACTGCTGCAATGAGACATTTGGCAGAGA 1197
D 1181 -----GAGGACTGCGCCTATGGCCACTTTGGTAGGGA 1213

RESULT 10
US-09-976-594-470
; Sequence 470, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 470
; LENGTH: 3495
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 2600262CB1
; NAME/KEY: unsure
; LOCATION: 2831-2993
; OTHER INFORMATION: a, t, c, g, or other
US-09-976-594-470

Query Match      28.3%; Score 420.8; DB 4; Length 3495;
Best Local Similarity 62.4%; Pred. No. 9.1e-120;
Matches 700; Conservative 0; Mismatches 407; Indels 15; Gaps 2;

QY 76 GGAGAGACATTCCTATTACCTCAGAGTCAGTGAAAGGAGACACCTCGACAAGCTCTG 135
D 156 GGAGGGCACATTCCTTTTCACTCAGAGTCGGTGGGGAAGGCCACCCAGATAAAGATTG 215

QY 136 CGACCAAACTCCGATGCTCTCGACGCTTGTGCTTGAACAGGACCCAGACAGCAAGT 195
D 216 TGACCAAAATCAGTATGCTGTCTTGTATGCCCCACTTCAGCAGGATCTCTGATGCCAAGT 275

QY 196 TGCTCGCAAAATGATGACCAAGACCAACTTTGTCATGCTTTCGGAGAGATTCACCA 255
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Db 276 AGCTTGGAACCTGTTGCTAAACCTGGAATGATCCTCTTCTGCTGGGAAATATACATCCAG 335  
Qy 256 GGCACACGTTGACTACGAGAAGATCGTGGGTGACACCTGCAGGAACATCGGCTTCGCTC 315  
Db 336 AGCTGCTGTTGACTACGAGAAGTGGTTCGTGAAGCTGTTAAACATTTGGATATGATCA 395  
Qy 316 AAACGATGTGGGACTTGATGCTGACAACTGCAAGTCCCTTGTGTAACATTTGAGCAGCAG 375  
Db 396 TTCTTCCAAAGGTTTGGACTACAAAGACTTGTAACTGCTGCTGCTGAGCCCTGGAGCAACGTC 455  
Qy 376 CCTCGATATTGCCACGCTGTGCACGCCACCTTTACCAAAAGACCCGAGGAATCGGTC 435  
Db 456 ACCAGATATTGCTCAAGGTG-----TCATCTTGACAGAAATGAAGAAGACATTTGTC 509  
Qy 436 TGGAGACCAAGGTCACATGTTTGGCTATGCCAGGACGAAACCCAGAAATTTGATGCCATT 495  
Db 510 TGGAGACCAAGGCTTAATGTTTGGCTATGCCACTGATGAACCTGAGGAGTGTATGCCCTT 569  
Qy 496 GAGTCATGTTTGGCAACTAAACCTCGGTGCTGCTCTCACCGAGTTTCGCAAGAACGGAAC 555  
Db 570 AACCAATTGCTTGGCACAAAGCTAAATGCCAACTGGCAGAACTACGCCGCTAATGGCAC 629  
Qy 556 CTGCCCATGTTGAGCGCTGTGGGAAACCCCAAGTGAAGTGTGATATTACAAATGACAA 615  
Db 630 TTTCGCTTGGTACGCGCTGATTTCTAAAACTCAAGTTACTGTGCAGTATATGCGAGATCG 689  
Qy 616 CGGTGCTGTTTCCAGTTTCGTGTCACACCTGTGCTTATCTCCACCAACATGATGAGAC 675  
Db 690 AGGTGCTGTGCTTCCATCAGAGTCCACAAATTTGTTATCTGTTGACATGATGAAGA 749  
Qy 676 TGTGACCAACGACGAAATTCAGCTGACCTCAAGGAGCATGTGATCAACCGCGTATCCC 735  
Db 750 GGTGTTGCTGTGATGAATGAGGATGCCCTTAAAGGAGAAAGTCAATCAAGACGATTTGTGC 809  
Qy 736 GGAGAGTACCTTGATGAGAGAACCAATTTTCATTTGAACCCCTCTGGCCGTTTGTCTAT 795  
Db 810 TCGGAAATACCTTGATGAGGATACAATCTACCACCTACAGCCAAAGTGGCAGATTTGTTAT 869  
Qy 796 TGGAGTCTCAGCGTGATGCTGCTCTCACCGGCCGCAAGATCATCATGATCTTACCG 855  
Db 870 TGGTGGCCCTCAGGCTGATGCTGTTGACTGGACGGAATAATCATTTGTCACACTTATGG 929  
Qy 856 AGGATGGGTGCTCATGTTGGTGGTCTTTCTCCGGAAGGATCCCAAGGTTGATAG 915  
Db 930 CGGTGGGTGCTCATGAGGAGGTGCTTTTCAGGAAAGGATTAATACCAAGGTGACCG 989  
Qy 916 GAGTGTGCTTACATTTGACAGACGCTGTAAGACATTTGGCAGTGGAGTAGCCAG 975  
Db 990 TTCAGCTGCTTATGCTGCTCGTTGGTGGCAAAATCCCTTGTAAAGGAGGCTCTGTGCG 1049  
Qy 976 AAGGTGCTATTGTGCAAGTGTCTTATGCCATTTGGTGGCCGAGCCCTTGTCTGCTTTGT 1035  
Db 1050 GAGGTTCTTGTTCAGTCTCTTATGCTATTTGAGTTCATCCATTAATCTATCTCCAT 1109  
Qy 1036 TGACACCTATGGCACCGGAAAGATCCATGATAGGAGATTTCAACATTTGTAAGAGAA 1095  
Db 1110 TTTCCATTAATGTTACCTCTCAGAAGAGTGAAGAGAGCTATTAGAGATTTGTAAGAGAA 1169  
Qy 1096 CTTTGTATTTAGCCCGGCTATGATCTCCATCAACCTTGTATCTCAGAGGGGTGGGATTA 1155  
Db 1170 TTTTCGATCTCCGCGCTGGGGTCAATTGTTCAGGGATCTGGATCTGAAAGAACCAATTATCA 1229  
Qy 1156 CAGGTTCTTTGAAGACTGTGCTATGACACTTTCCGACAGAA 1197  
Db 1230 -----GAGGACTGACGCTTATGGCCACTTTTGTAGGGA 1262

RESULT 11  
US-09-949-016-1787  
; Sequence 1787, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1787  
; LENGTH: 3220  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-1787

Query Match 27.7%; Score 411.4; DB 4; Length 3220;  
Best Local Similarity 62.5%; Pred. No. 7,3e-117;  
Matches 662; Conservative 0; Mismatches 391; Indels 6; Gaps 1;

Qy 86 TTCCTATTACTCAGAGTCAGTGAACGAGGGACACCTCTGACAAAGCTCTGCCAACCAATC 145  
Db 123 TTCAATGTTTCAATCGAGTCTGTGGAGAGGGACACCCGGATAAGATCTGTGACCGAGATC 182  
Qy 146 TCCGATGCTGCTCGACGCTTGCTTGAACAGGACCCAGACAGCAAGGTTGCCCTGCGAA 205  
Db 183 AGTGATGAGTGTGATGCCATCTCAAGCAAGACCCCAATGCCAAGGTGCTGTGAG 242  
Qy 206 ACATGCACCAAGACCAACTTGTGTCATGCTCTTCCGAGAGATCAACCAAGGCCAACGTT 265  
Db 243 ACAGTGTGCAAGACCGGCATGCTGCTGTGTGTGAGATCACCTCAATGCCATGGTG 302  
Qy 266 GACTACGAGAGATCGTGGTGACACCTGTCAGGAAACATCGGCTTGTCTCTAAACGATGTG 325  
Db 303 GACTACACGCGGTGTGGAGGACACCATCAAGCAACATCGGCTACGATGACTCAGCCCAAG 362  
Qy 326 GGACTTGATGTCACAACTGCAAGGTCCTGTGTAACATTTGAGCAGCAGACCCCTGATATT 385  
Db 363 GCTTTGACTTCAGACTTTGCAACGCTGCTGTGGCTTTGGAGCAGCAATCCCGCATATT 422  
Qy 386 GCCAGGGTGTGCACGGCCACCTTACCAAAAGACCCGAGGAAATCGGTGCTGGAGACCAAG 445  
Db 423 GCCCAGTG-----CGTCCATCTGGAAGAAATGAGGAGGATGTGGGGCAGGAGATCAG 476  
Qy 446 GGTCACTGTTTGGCTATGCCAGGACCAACCCAGAAATTTGATGATGCCATTTGATGATGTT 505  
Db 477 GGTGATGTTTGGCTATGCTACCGACGAGACAGAGGAGTGCATGCCCTTCAACCATCATC 536  
Qy 506 CTTGCAACTAAACTCGGTGCTGCTCTCACCGAGGTTCCGAAGACGGAACCTGCCCATGG 565  
Db 537 CTTGCTCAAGCTCAACGCCGGATGGCAGACCTCAGCGGCTCCGGGCTCTCCCTCGG 596  
Qy 566 TTGAGCCCTGATGGGAAACCCCAAGTGAAGTGTGAGTATTACAAATGACAAAGGTGCCATG 625  
Db 597 CTGGGCTGACTCTAAGACTCAGGTGACAGTTTCAGTACATGTCAGGACAAATGGGCGAGTC 656  
Qy 626 GTTCAGTTCGTGTCCACACTGTGTTATCTCCACCCCAACATGATGAGACTGTGACCAAC 685  
Db 657 ATCCCTGTGCGCATCCACACCATCTGTCATCTCTGTGACGACCAACGAAGACATCATCGCTG 716  
Qy 686 GACGAAATTCAGCTGACCTCAAGGAGCATGTGATCAAGCCGCTGATCCCGAGAGATAC 745  
Db 717 GAGGAGTGGCAGGGCCCTGAAGAGCAAGTCAATCAGGGCGGTGTCGCGGCCAAGTAC 776  
Qy 746 CTTGATGAGAAAGACCAATTTTCCACTTGAACCCCTCTGGCCGCTTTTGTCTCATTTGAGGCTCT 805  
Db 777 CTGGACGAAGACACCGTCTACACCTGTCAGCCCGCTGAGGCGGCTTTGTCTATCGGAGGTCCC 836  
Qy 806 CACGCTGATGCTGTCTCACCGCGCGGAAGATCATCATGATCTTACGAGGATGGGT 865



Db 837 CAGGGGATGCGGGTGTCTACTGGCCGTAAAGATTATTGTGGACACCTATGCGCGCTGGGG 896  
Qy 866 GTCATATGTTGGTGGTCTTTCTCCGGGAAGAGATCCACCAAGTTGATAGAGTGGTCT 925  
Db 897 GCTCATGTTGGTGGGCGCTTCTCTGGGAAGGACTACACCAAGTGGACCGCTCAGCTGCA 956  
Qy 926 TACATTTGAGACAGCGCTCTAAGACATTTGGCAGTGGAGTGGACTAGCAGAGGTGCATT 985  
Db 957 TATGTCGCCGTGGGTGGCCCAAGTCTCTGGTGAAGCAGGGCTCTGCGGAGAGTGTCT 1016  
Qy 986 GTGCAAGTGTCTTATGCCATTTGGTGGCCGAGCGCTTTGTCTGTCTTTGTGACACCTAT 1045  
Db 1017 GTCCAGTTTCTATGCCATTTGGTGGCCGAGCGCTGTCCATTTCCACTTTCACCTAC 1076  
Qy 1046 GGCACCGGAAGATCATGATTAAGAGATTTCTCAACATTTGGAAGAGAACTTTGATTTC 1105  
Db 1077 GGAACCTCTCAGAAGACAGAGAGAGCTGCTGGATGTGGTGCATAAAGAACTTCGACCTC 1136  
Qy 1106 AGGCCGGTATGATCTCCATCAACCTTGATCTCAGAGG 1144  
Db 1137 CCGCCGGCGCTCATTTGTCTAGGATTTGGACTTTGAAGAAG 1175

RESULT 12  
US-09-318-448-20  
; Sequence 20, Application US/09318448  
; Patent No. 6210950  
; GENERAL INFORMATION:  
; APPLICANT: Stentors, William G.  
; APPLICANT: Johnson, Edward S.  
; TITLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND TREATING  
; TITLE OF INVENTION: DEVELOPMENTAL DISORDERS  
; FILE REFERENCE: 601-1-057  
; CURRENT APPLICATION NUMBER: US/09/318,448  
; CURRENT FILING DATE: 1999-05-25  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 3228  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-318-448-20

Query Match 27.7%; Score 411.4; DB 3; Length 3228;  
Best Local Similarity 62.5%; Pred. No. 7.3e-117;  
Matches 662; Conservative 0; Mismatches 391; Indels 6; Gaps 1;

Qy 86 TTCTATTATCTCAGAGTCAGTGAACGAGGACACCCCTGCAAGCTCTGCGACCAAAATC 145  
Db 123 TTCATGTTACATCGGAGTCTGTGGAGAGGACACCCGGATGAATCTGTGACCAAGATC 182  
Qy 146 TCCGATGTCCTCGACGCTTCCCTTGAACAGGACCCAGACAGCAAGGTTGCTGCGAA 205  
Db 183 AGTGATGCAAGTGTGGATGCCATCTCAAGCAAGACCCCAATGTCCAAGTGGCTGTGAG 242  
Qy 206 ACATGACCAAGACCACTGTGTCTGTGAGAGATCACCACCAAGGCCCAAGCTT 265  
Db 243 ACAGTGTGAAGACCGGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 302  
Qy 266 GACTAGGAAGATCGTGGTGACACCTCAGGACATCGGCTTCGTCTCAAAAGCATGTG 325  
Db 303 GACTACACGGGTGTGAGGACACCATCAAGACATCGGTGATGATGATGATGATGATGATG 362  
Qy 326 GGAATTGATGTCACAACTGCAAGGTCCTTTGTAACATTTGACAGCAGAGCCCTGATTT 385  
Db 363 GCGTTTGACTTCAAGACTTGAACGTCGTGGTGGCTTTGGAGCAGCAATCCCAATATT 422  
Qy 386 GCCCGGTGTGACGGCCACCTTACCAAAAGACCCGAGGAATCGGTGCTGGAGACGAG 445  
Db 423 GCCCAGTG-----CGTCCATCTGGACAGAAATGAGGAGGATGTGGGGCAGGATCAG 476  
Qy 446 GGTTCATGTTTGGCTTATGCCAGGACGAAACCCAGAAATGATGCTTGTGATGATGTT 505

Db 477 GGTTTGATGTTCCGCTATGCTACCGACGACAGAGAGTGCATGCCCTCACCATCATC 536  
Qy 506 CTTGCAACTAACTCGGTGCTGTCTCACGAGGTTTGGCAAGAAACGGAACCTGCCCCATGG 565  
Db 537 CTTGCTCAAGCTCAACGCGCGGATGGCAGACCTCAGGCGCTCCGCGCTCTCCCTCGG 596  
Qy 566 TTGAGGCTGATGGGAACCCCAAGTGAATGTTGAGTATTACATGACAAAGGTTGCCATG 625  
Db 597 CTGCGGCTGACTTAAGACTCAGTGACATCAGTACATGTCAGGACAAATGGCGCAGTC 656  
Qy 626 GTTCAGTTCGTGCCACATCTTATCTCCACCCCAACATGATGAGACTGTGACCAAC 685  
Db 657 ATCCCTGTGCGATCCACACCATCGTCATCTCTGTGAGCACAAGAGACATCAGCGTG 716  
Qy 686 GACGAATTTGAGTGACCTCAAGAGCATGTGATCAAGCCGCTGATCCCGGAGAGATAC 745  
Db 717 GAGGAGATGCGCAGGGCCCTGAAGAGCAAGTCACTAGGCGCGTGGTGGCCGCAAGTAC 776  
Qy 746 CTTGATGAGAAGACATTTTCCACTTGAACCCCTCTGCGCGTGTGTGATTTGGAGGTCT 805  
Db 777 CTGACGGAAGACACCGTCTACCACTGACGCCAGTGGCGGTGTGTCTATCGGAGGTCCC 836  
Qy 806 CACGTGATGCTGTCTCACCGCGCGAAGATCATCATCTTACGAGAGGATGGGCT 865  
Db 837 CAGGGGATGCGGTGTCTACCTGCGCTAAGATTATTTGGACACCTATGCGCGCTGGGG 896  
Qy 866 GCTCATGTTGTTGTTCTTCCGGGAAGATCCCAAGGTTGATAGAGTGGTGTCT 925  
Db 897 GCTCATGTTGTTGTTCTTCTCTGGGAAGACTACACCAAGGTAGACCGCTCAGCTGCA 956  
Qy 926 TACATTTGAGACAGGCTGCTAAGAGCATTTGTGCAAGTGGAGTGGACTAGCAGAGGTGCATT 985  
Db 957 TATGTCGCCCTGGGTGGCCCAAGTCTCTGTGAAAGCAGGGCTCTGCGGAGAGTGTCT 1016  
Qy 986 GTGCAAGTGTCTTATGCAATTTGTGCGCGAGCTTTGTCTGTCTTTGTTGACACCTAT 1045  
Db 1017 GTCCAGTTTCTATGCCATTTGTGTGCGCGAGCGCTGTCCATTTCCATCTTCCCTAC 1076  
Qy 1046 GGCACCGGAAGATCCATGATAAGAGATTCTCAACATTTGTAAGAGAGAACTTTGATTT 1105  
Db 1077 GGAACCTCTCAGAAGACAGAGCAGAGCTGTGATGTTGTTGTCATAGAACTTCGACCTC 1136  
Qy 1106 AGGCCGGTATGATCTCCATCAACCTTGATCTCAGAGG 1144  
Db 1137 CCGCGGCGTCTATGTCAGGAGTTTGGACTTTGAAGAAG 1175

RESULT 13  
US-09-949-016-68  
; Sequence 68, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USBS THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 68  
; LENGTH: 3228  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-68  
Query Match 27.7%; Score 411.4; DB 4; Length 3228;



Best Local Similarity 62.5%; Pred. No. 7.3e-117;  
Matches 662; Conservative 0; Mismatches 391; Indels 6; Gaps 1;

QY 86 TTCTATTACCTCAGAGTCAGTGAACGAGGGACACCTGACAAAGCTCTGCGACCAATC 145  
DB 123 TTCTATTACCTCAGAGTCAGTGAACGAGGGACACCTGACAAAGCTCTGCGACCAATC 182  
QY 146 TCCGATGCTGCTCGACGCTTCCCTTGAACAGGACCCAGACAGCAAGGTTGCTCGAA 205  
DB 183 AGTGATGCACTGCTGATGCCATCTCAAGCAAGACCCCAATGCCAAGTGGCTGTGAG 242  
QY 206 ACATGACCAAGACCACTTGGTCATGCTTCCGAGAGATCAACCAAGGCCACGTT 265  
DB 243 ACAGTGTGCAAGACCCGCGATGCTGCTGTGTGTGAGATCACTCAATGGCCATGGTG 302  
QY 266 GACTACGAGAAGATCGTGGTGACACTCGCAGCAACATCGGCTTCGTCTCAACAGATGG 325  
DB 303 GACTACAGCGGTGTGAGGACACATCAACACATCGGCTTACGATGACTCAGCAAG 362  
QY 326 GGAATTGATGCTGACAACTGCAAGGTCTTGTAAACATTTGAGCAGCAGACCCCTGATAT 385  
DB 363 GGCTTTGACTTCAAGACTTGCACAGTGTGCTGCTTGGAGCAGCAATCCCGAGATAT 422  
QY 386 GCCCAGGTGTGACCGGCACTTACAAAGACCCGAGGAATCGGTGTGAGACCAAG 445  
DB 423 GCCCAGTG-----CGTCCATCTGGAACAGAAATGAGGAGATGTGGGGCAGGATCAG 476  
QY 446 GGTTCATGTTTGGCTATGCCAGGACGAAACCCAGAAATGATGCAATGATGATGATGTT 505  
DB 477 GGTTCATGTTTGGCTATGCTACCGAGCAGACAGAGGATGATGCTCCCTCCACATCATC 536  
QY 506 CTTGCAAACTAAACTCGGTGTCTGCTCACCGAGTTTCGAAAGACCGAACCTGCCCATGG 565  
DB 537 CTTGCTCACAAGCTCAAGCCCGGATGGCAGACCTCAGGGCTCCGCTCTCCCTCGG 596  
QY 566 TTGAGCGCTGATGGGAAACCCAGTGACTGTTGAGTATTAATGACAAAGGTGCCATG 625  
DB 597 CTGCGCCTGACTCTAAGACTCAGGTGACAGTTTCACTATGACGAGCAATGCGCAGTC 656  
QY 626 GTTCCAGTTTGTGTCACACTGTCTTATCTCCACCCCAACATGATGAGACTGTGACCAAC 685  
DB 657 ATCCCTGTGGGATCACAACACTCGTCTATCTGTGAGCAACCAAGACATCAAGCTG 716  
QY 686 GAGCAAAATTCAGCTCAGCTCAAGGAGCATGTGATCAAGCCGCTGATCCCGGAGAGTAC 745  
DB 717 GAGGATGCGCAGGCGCTGAGGAGCAAGTCACTCAGGGCGTGTGCGCGGCAAGTAC 776  
QY 746 CTTGATGAGAAGACCAATTTTCCACTTGAACCCCTCTGGCGGTTTGTCAATGGAGTCT 805  
DB 777 CTGACGAAAGACACCGCTTACCACTGACCCCAAGTGGCGGTTTGTCAATCGAGGTCC 836  
QY 806 CAGGTGATGCTGCTCACCGGCGCAAGATCATCATGATCATCTTACGAGGATGGGT 865  
DB 837 CAGGGGATGCGGGTGTCACTGGCCGTAAGATTAATTTGGACACCTTATGGCGGTGGGG 896  
QY 866 GCTCATGCTGCTGCTTTCTCCGGAAGGATCCCAAGGTTTATAGGAGTGTGCT 925  
DB 897 GCTCATGCTGCTGCTTTCTGGAAGGACTACCAAGGTAGACCGCTCAGCTGCA 956  
QY 926 TACATTTGAGACAGGCTGTGAAGACATTTGGGCAAGTGGACTAGCCAGAGAGTGCAT 985  
DB 957 TATGCTGCCGCTGGGTGGCAAGTCTCTGGTGAAGCAGGGCTCTGCGCGAGAGTGCCT 1016  
QY 986 GTGCAAGTGTCTTATGCCATGGGTGGCGGCTTGTCTGTCTTGTGACACCTAT 1045  
DB 1017 GTCAGGTTTCTTATGCCATGGGTGGCGGCGCTGTCCATTTCCATCTTCACTTAC 1076  
QY 1046 GGCACCGGGAAGATCCATGATAGGAGATTTCTCAACATTTGTGAAGGAGAACTTTGAT 1105  
DB 1077 GGNACCTCTCAGAGACAGCGAGAGCTGCTGGATGTGTGATAGAACTTGGACCTC 1136  
QY 1106 AGCCCGGTATGATCTCCATCAACCTTTGATCTCAAGAGG 1144

DB 1137 CGGCCGGCGTCAATTGTTCAGGATTTGGACTTTGAAGAAG 1175

RESULT 14  
US-09-248-796A-4152  
; Sequence 4152, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS  
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; PRIOR FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 4152  
; LENGTH: 1173  
; TYPE: DNA  
; ORGANISM: Candida albicans  
; US-09-248-796A-4152

Query Match 25.9%; Score 384.8; DB 4; Length 1173;  
Best Local Similarity 61.0%; Pred. No. 6.8e-109;  
Matches 645; Conservative 0; Mismatches 407; Indels 6; Gaps 1;

QY 80 GAGACATTCCTATTATTCCTCAGAGTCAGTGAACGAGGGACACCTGACAAAGCTCTGCGAC 139  
DB 31 GAAACTTTCTCTTTTCACTTTCAGATCCGTTGGTGAAGGTCAACAGATAAGATTTGTGAC 90  
QY 140 CAAATCTCCGATGCTGCTCGACGCTTGCCTTGAACAGGACCCAGACAGCAAGTTGCC 199  
DB 91 CAACTCTCCGATGCCATTTAGATGCTTGTAGCTTGTATGCTTGTCAAAAGTTGCT 150  
QY 200 TCGCAAAACATGACCAAGACCAACCTTGGTCATGCTTTCGGAGAGATCAACCAAGGCC 259  
DB 151 TGTGAACCTGCTGCCAAACCGGTATGATGTTTGTGTAATTTACCACTAAAGCT 210  
QY 260 AACGTTGATGACGAGAAGATGCTGTCAGACCTGACAGCAATCGGCTTGTCTCAAAAC 319  
DB 211 CAAATGGATTTATCAAAAATCATTAGAGACACCATTAACACATTTGGTTACGACGATTC 270  
QY 320 GATGTTGGACCTTGTGCTGACAACTGCAAGGTCCTTGTAAACATTTGAGCAGCAGACCT 379  
DB 271 GAAAAGGTTTGTATACAGACTTGTAACTGTTGCTTGTGCAATTTGAACACAACTCTCA 330  
QY 380 GATATTGCCAGGTTGTGACGCGCCACCTTACCAAAAGACCCGAGGAAATCGGTGCTGA 439  
DB 331 GATATTGCTCAAGGTTTACATTTACGA-----AAAAAGCTTTTGAAGAGTTGGGTGCTGT 384  
QY 440 GACCAAGGTGACATGTTGGCTATGCCAGGACGAAACCCCAAGATTTGATGCAATGAGT 499  
DB 385 GATCAAGGTATTTATGTTGGTTATGCCACCGATGAACCGATGAAAAATTTGCCATTTGACC 444  
QY 500 CATGTTCTTGCAACTAAACTCGGTGCTGCTCACCGAGTTTCGCAAGAACGGAACCTGCG 559  
DB 445 ATTTATTGGGCCCAAAATTTGATGCTGCTTGGCTTCTGCCAAGAGATCAGGTTCTCTTG 504  
QY 560 CCATGTTTGAGGCTGTATGGGAAAAACCAAGTGACTGTTGAGTATTTACAATGACAACTGT 619  
DB 505 CCATGTTTGAGACCAAGATACCAAAACCAAGTCAACCATCGAGTATGAAAGATGTTGCT 564  
QY 620 GCCATGTTTCCAGTTGCTGTCACACTGTGTTATCTCCACCAACATGATGAGACTGTG 679  
DB 565 GCAGTTATCCCAAAAAGAGTCGACAAATTTGTTATTTCCACTCAACATGCGCCGAGAAATC 624  
QY 680 ACCACGACGAAATTTGACGCTGACCTCAAGGAGCATGTGATCAAGCCGCTGATCCCGAG 739  
DB 625 ACCACCGAAATTTGAGAAAAAATTTTGAACATATCATCAAGCAAGATCATCCAGAA 684

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QY 740 AAGTACCTTGATGAGNAGACCAATTTTCCACTTGAACCCCTCGGCGGTTTGTCTATTGA 799
Db 685 CATTTATTAGACGACAAAATCTATACCAATTCAGCCATCAGGAGATTCGTCAATGGT 744
QY 800 GGTCTCTACGGTGATGCTGGTCTCACGGCCGCAAGATCATCATCGATACCTTACGGAGGA 859
Db 745 GGTCCCAAGGTGATGCTGGTGTGACTGTAGAGAGATCATTTGTGACACCTATGGTGT 804
QY 860 TGGGTGCTCATGGTGGTGGTGGTCTTCTCCGGGAAGGATCCACCAAGTTGATAGGAT 919
Db 805 TGGGGCGCACATGGTGGTGGTGGTCTCTCAGGCAAGGATTTCTCAAAGTTGATAGGCT 864
QY 920 GGTGCTTACATTTGTGACAGAGCTGCTAAGACATTTGGCAAGTGGAGTACGACGAGAAG 979
Db 865 GGTGCTTATGCGCGCTGGTGGTGGTGGCAAGTGGTGGTGGACCGCCGATTTGCCCAAAAG 924
QY 980 TGCATTGTGCAAGTGTCTTATGCAATTTGGTGTGCGCGAGCCTTTGTCTGTCTTGTGAC 1039
Db 925 GCTTGGTGCAGTTCTCTATGCTATTTGGGTGTGTAACCCACCAACATTTATATAGAC 984
QY 1040 ACCTATGGCACCGGGAAGATCCATGATAAGAGATTTCTCAACATTTGTGAAGAGAACTTT 1099
Db 985 ACCTATGGGACATCTAAATTTAGACACCGAAGCCCTTGTAGAAATTTATCAAGAAATAATTT 1044
QY 1100 GATTTGAGCCCGGTATGATCTCCATCAACCTTGATCT 1137
Db 1045 GACTTACGCCCTGGCGTAATTTGTAAGAAATTAGATTT 1082

RESULT 15
US-09-489-039A-4746
; Sequence 4746, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIORITY FILING DATE: 2000-01-27
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 4746
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-4746
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Best Local Similarity 57.9%; Pred. No. 1.3e-84;
Matches 595; Conservative 0; Mismatches 412; Indels 21; Gaps 2;
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QY 143 ATCTCCGATGCTGTCTCTCGACGCTTGCCTTTGAACAGGACCCAGACAGCAAGGTTGCTGC 202
Db 70 ATCTCCGATGCTGTCTCGATGCGATCTCTCGAGCAGGATCCGAAAGCGGTGTGTCATGT 129
QY 203 GAAACATGCCACNAGACCAACTTGGTCATGGTCTTCGGAGAGATCACCACCAAGGCCAAC 262
Db 130 GAAACCTATTTGTAACAAACCGGCATGGTGGTGGTAGGCGCGAATCACCACCAAGCATGG 189
QY 263 GTTGACTACGAGAAGATCGTGGTGACACCTGAGGAACATCGGCTTTCGTCTCAACACGAT 322
Db 190 GTTGATATCGAGAGATCACCAGCAACCGTCCGGAATTTGGCTACGTGCAATTCGGAT 249
QY 323 GTGGGACTTGATGCTGACAACTGCAAGGTCCTTTGTAACAATTTAGACAGACGCGCTGAT 382
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Db 310 ATTAACAGGGCGGTGACCGGTGCCGAT-----CGGTGGAAACAGGGCGCGCGGAC 360
QY 443 CAGGGTCACATGTTTGGCTATGCCACGACGAAACCCAGAAATTCATGCCATTCAGTGCAT 502
Db 361 CAGGGCTGATGTTTGGCTACGCCACTAAAGAAACCGACGTGCTGATGCCGGCGCGGTG 420
QY 503 GTTCTTGCAACTAACTCGGTGCTCGTCTACCGAGGTTCCGAAAGACGGAACCTGCCCA 562
Db 421 ACTTACGCTCACCGTCTGGTGCAGGCTCAGGCTGAAAGTGGCTTAAACCGCACCTGCGG 480
QY 563 TGGTTGAGGCTGATGGGAAACCCAGTGAATCTTGAATATTACAAATGACAAACGAGTCC 622
Db 481 TGGCTGCGCCCGGATGCGAAAGCCAGGTGACCTTCCAGTATGACGCGGCAAAATTCGTC 540
QY 623 ATGGTTCCAGTTCGTGTCACACTGTGCTTATCTCCACCCCAACATGATGAGACTGTGACC 682
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QY 683 AACGACGAAATTCAGCTGACCTCAAGAGCATGTGATCAAGCCGGTGTATCCCGAGAAG 742
Db 589 CAGAAATCCCTGCAGGAAGCAGTGTGAGAGAGATCATCAAGCCGATTTCTGCCGACCGAA 648
QY 743 TACCTTGATGAGAAGACCATTTTCCACTTGAACCCCTCTGGCGGTTTTGTTCATTGGAGGT 802
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Db 709 CGGATGGCGACTGCGGTCTGACCGTCTGTAAGATCATCGTTGATACCTACGGGCGCATG 768
QY 863 GGTGCTCATGTGTGTGGTGTCTTCTCCGGGAAGGATCCACCAAGGTTGATAGGAGTGT 922
Db 769 GCTGCCACGCGCGCGCGCTTCTCCGTTAAAGATCCATCTAAAGTTGACCGTTCCGCA 828
QY 923 GCTTACATTTGACACAGGCTGCTAAGAGCATTTGGCAAGTGGACTAGCCAGAGGTGC 982
Db 829 GCCTACGCGCGCGCTATGTGGCAAGAACATCGTTGCCGAGGCTTGGCGCATGCTTGC 888
QY 983 ATTGTGCAAGTGTCTTATGCAATTTGGTGTGCCCGAGCCTTTGTCTGCTTTTGTGACACC 1042
Db 889 GAAATTCAGGTTTCTACGCTATCGCGTTTCAGAACCGACGTCATCATGTGTGAAACC 948
QY 1043 TATGACCCGGAAGATCCATGATAAGAGATTTCTCAACATTTGAGAGGAACTTTGAT 1102
Db 949 TTGGCACCGAGAAAGTGCCTTCTCAACAGCTGACCCCTGCTGGTGGTGGTGTCTTCGAC 1008
QY 1103 TTCAGGCC 1110
Db 1009 CTGCGTCC 1016
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Search completed: August 31, 2005, 06:13:11
Job time : 254.414 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 30, 2005, 21:30:39 ; Search time 995.128 Seconds  
(without alignments)  
9764.058 Million cell updates/sec

Title: US-10-734-698A-38  
Perfect score: 1485  
Sequence: 1 ACCCAAGCCCACTCAACCA.....CAAAAAGATGTTCCAGTT 1485

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 7331713 seqs, 3271544945 residues

Total number of hits satisfying chosen parameters: 14663426

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA.\*

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26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	1485	100.0	1485	20	US-10-734-698A-38
2	1485	100.0	1485	21	US-10-917-602A-38
3	1485	100.0	1518	17	US-10-431-252-1
4	1474.6	99.3	1496	18	US-10-425-114-11983
5	1464.6	98.6	1855	18	US-10-424-599-77204
6	1460.2	98.3	1465	18	US-10-425-114-10164
7	1208.6	81.4	1538	18	US-10-424-599-115395

8	1207.6	81.3	1509	18	US-10-425-114-39554	Sequence 29554, A
9	1205.2	81.2	1210	18	US-10-425-114-7305	Sequence 7305, Ap
10	1204.4	81.1	1488	18	US-10-425-114-7202	Sequence 7202, Ap
11	1204.4	81.1	1494	18	US-10-425-114-10112	Sequence 10112, A
12	1204.4	81.1	1505	18	US-10-425-114-11712	Sequence 11712, A
13	1204.4	81.1	1510	18	US-10-425-114-11050	Sequence 11050, A
14	1204.4	81.1	1514	18	US-10-425-114-8323	Sequence 8323, Ap
15	1204.4	81.1	1514	18	US-10-425-114-9591	Sequence 9591, Ap
16	1204.4	81.1	1514	18	US-10-425-114-10155	Sequence 10155, A
17	1204.4	81.1	1514	18	US-10-425-114-10248	Sequence 10248, A
18	1204.4	81.1	1515	18	US-10-425-114-8286	Sequence 8286, Ap
19	1204.4	81.1	1515	18	US-10-425-114-8296	Sequence 8296, Ap
20	1204.4	81.1	1515	18	US-10-425-114-9070	Sequence 9070, Ap
21	1204.4	81.1	1515	18	US-10-425-114-9087	Sequence 9087, Ap
22	1204.4	81.1	1515	18	US-10-425-114-9138	Sequence 9138, Ap
23	1204.4	81.1	1515	18	US-10-425-114-11285	Sequence 11285, A
24	1204.4	81.1	1515	18	US-10-425-114-12737	Sequence 12737, A
25	1204.4	81.1	1515	18	US-10-425-114-12745	Sequence 12745, A
26	1204.4	81.1	1523	18	US-10-425-114-10819	Sequence 10819, A
27	1204.4	81.1	1529	18	US-10-425-114-10266	Sequence 10266, A
28	1204.4	81.1	1529	18	US-10-425-114-12664	Sequence 12664, A
29	1202.8	81.0	1515	18	US-10-425-114-10041	Sequence 10041, A
30	1196.6	80.6	1495	18	US-10-425-114-10262	Sequence 10262, A
31	1195	80.5	1835	18	US-10-424-599-77205	Sequence 77205, A
32	1192.2	80.3	1489	18	US-10-425-114-7368	Sequence 7368, Ap
33	1191	80.2	1427	18	US-10-425-114-12787	Sequence 12787, A
34	1191	80.2	1458	18	US-10-425-114-8399	Sequence 8399, Ap
35	1191	80.2	1458	18	US-10-425-114-8336	Sequence 8336, Ap
36	1191	80.2	1461	18	US-10-425-114-8325	Sequence 8325, Ap
37	1191	80.2	1461	18	US-10-425-114-11194	Sequence 11194, A
38	1191	80.2	1468	18	US-10-425-114-10273	Sequence 10273, A
39	1189.4	80.1	1456	18	US-10-425-114-10701	Sequence 10701, A
40	1175.4	79.2	1459	18	US-10-425-114-9680	Sequence 9680, Ap
41	1145	77.1	1349	18	US-10-425-114-11199	Sequence 11199, A
42	1142.6	76.9	1349	18	US-10-425-114-11868	Sequence 11868, A
43	1132.8	76.3	1342	18	US-10-425-114-8517	Sequence 8517, Ap
44	1124.4	75.7	1436	18	US-10-424-599-77201	Sequence 77201, A
45	938.2	63.2	1084	18	US-10-425-114-8006	Sequence 8006, Ap

#### ALIGNMENTS

#### RESULT 1

US-10-734-698A-38  
; Sequence 38, Application US/10734698A  
; Publication No. US20040209341A1

#### GENERAL INFORMATION:

APPLICANT: FALCO, SAVERIO CARL  
ALLEN, STEPHEN M.  
RAFALSKI, J. ANTONI  
HITZ, WILLIAM D.  
KINNEY, ANTHONY J.  
ABELL, LYNN N.  
THORPE, CATHERINE J.

TITLE OF INVENTION: PLANT AMINO ACID BIOSYNTHETIC ENZYMES

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY  
STREET: 1007 MARKET STREET  
CITY: WILMINGTON  
STATE: DELAWARE  
COUNTRY: USA  
ZIP: 19898

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.50 INCH

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: MICROSOFT WINDOWS 95

SOFTWARE: MICROSOFT WORD VERSION 7.0A

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/734,698A

FILING DATE: 12-Dec-2003

CLASSIFICATION: <Unknown>













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Db 609 GCAAGACGAACTGCCCATGGTTGAGCGCTGATGGGAGACCCAGTGACTGTTGAGT 668  
QY 603 ATTACAATGACAAACGGTGCCATGGTTCCAGTTGCTGTCACACTGTGCTTATCTCCACC 662  
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QY 663 AACATGATGAGACTGTGACCAACGAGCAAAATTTGAGCTGACCTCAAGGAGCATGTGATCA 722  
Db 729 AACATGATGAGACTGTGACCAACGAGCAAAATTTGAGCTGACCTCAAGGAGCATGTGATCA 788  
QY 723 AGCCGGTGATCCCGAGAGTAGTACCTTGATGAGAAGACCAATTTCCACTTTGAACCCCTCTG 782  
Db 789 AGCCGGTGATCCCGAGAGTAGTACCTTGATGAGAAGACCAATTTCCACTTTGAACCCCTCTG 848  
QY 783 GCCGTTTGTCTCATTTGAGAGTCTCAAGGTGATGCTGCTGTCTCAAGGAGCATGTGATCA 842  
Db 849 GCCGTTTGTCTCATTTGAGAGTCTCAAGGTGATGCTGCTGTCTCAAGGAGCATGTGATCA 908  
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Db 1089 TGTCTGTCTTTGTCGACCTTATGGCAGCGGAGATCCATATAGGAGATTCTCAACA 1148  
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Db 1149 TTGTGAAGGAGAACTTTGATTTTCAAGCCCGGTATGATCTCCATCAACCTTTGATCTCAAGA 1208  
QY 1143 GGGGTGGGAATTAACAGGTTCTTGAAGACTGTGTCATATGAGACACTTTGGCAGAGAGGACC 1202  
Db 1209 GGGGTGGGAATTAACAGGTTCTTGAAGACTGTGTCATATGAGACACTTTGGCAGAGAGGACC 1268  
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Db 1269 CTGACTTCATCATGGGAGGTGTCACGCCCTCAAGTGGGAGAGGCTTAAGGCCATTCTAT 1328  
QY 1263 TCACCTGCAATGTGCTGGGAGTTTTTTAGCGTTGGCCCTTATATGTCTATTATCCATTAAC 1322  
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RESULT 6  
US-10-425-114-10164  
; Sequence 10164, Application US/10425114  
; Publication No. US2004003488A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jindong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E

; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425.114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 10164  
; LENGTH: 1465  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700896469\_FLI  
US-10-425-114-10164

Query Match 98.3%; Score 1460.2; DB 18; Length 1465;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1462; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 1 CCACACCACTCTCTGCTCTTCTTACCTTCAAGTTTAAAGTATTAAAGTGGCAG 60  
QY 81 AGACATTCTTACCTCAGAGTCAGTGAACGAGGACACCCCTGACAGCTCTCGACC 140  
Db 61 AGACATTCTTACCTCAGAGTCAGTGAACGAGGACACCCCTGACAGCTCTCGACC 120  
QY 141 AAATCTCGATGCTGCTCTCGACGCTTGTGAACAGAGCCAGACAGCAAGGTTGCT 200  
Db 121 AAATCTCGACGCTGCTCTCGACGCTTGTGAACAGAGCCAGACAGCAAGGTTGCT 180  
QY 201 GCGAAACATGACCAAGACCACTTGTGTCAGTCTCGAGAGATCACCAAGAGGCA 260  
Db 181 GCGAAACATGACCAAGACCACTTGTGTCAGTCTCGAGAGATCACCAAGAGGCA 240  
QY 261 ACCTTGACTACGAGAAAGATCGTGTGTCACCTCGAGGAACATCGCTTCTCAAAG 320  
Db 241 ACCTTGACTACGAGAAAGATCGTGTGTCACCTCGAGGAACATCGCTTCTCAAAG 300  
QY 321 ATGTGGGACTTGAATGCTGACAACTGCAAGGTCCTTGTAAAACATTGAGCAGAGCCCTG 380  
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QY 381 ATATTTGCCAGGTGTGACCGCCCACTTACCAAAAGACCCGAGGAATCGTGTCTGGAG 440  
Db 361 ATATTTGCCAGGTGTGACCGCCCACTTACCAAAAGACCCGAGGAATCGTGTCTGGAG 420  
QY 441 ACCAGGGTCACATGTTTGGCTATGCGACGAGAAACCCAGAAATTGATGCCATTGAGTC 500  
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QY 621 CCATGTTTCCAGTTCTGTTCCACACTGTGCTTATCTCCACCAACATGATGAGCTGGA 680  
Db 601 CCATGTTTCCAGTTCTGTTCCACACTGTGCTTATCTCCACCAACATGATGAGCTGGA 660  
QY 681 CCAACGAGAAATTGACGTCGACCTCAAGGAGCATGTGATCAAGCCGGTATCCCGAGA 740  
Db 661 CCAACGAGAAATTGACGTCGACCTCAAGGAGCATGTGATCAAGCCGGTATCCCGAGA 720  
QY 741 AGTACCTTGAAGAGACCAATTTTCCACTTGAACCCCTCTCGCCGTTTTTGTTCATTTGAG 800  
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QY 1170 CTGCTGATATGACACTTCGGCAGAGAGACCTTGACTTCACATGGGAAGTGGTCAAGC 1229
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Db 1432 GATCAATTCAACGTGATAC 1450

RESULT 8
US-10-425-114-29554
; Sequence 29554, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 29554
; LENGTH: 1509
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-GMFLMINSOY064D01_FLI
US-10-425-114-29554

Query Match 81.3%; Score 1207.6; DB 18; Length 1509;
Best Local Similarity 92.0%; Pred. No. 0;
Matches 1345; Conservative 0; Mismatches 99; Indels 18; Gaps 6;

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QY 89 CTATTTTACCTCAGAGTCAGTGAACGAGGACACCTTGCAAGCTCTGCGACCAATCTCC 148
Db 104 CTATTTTACCTCAGAGTCAGTGAACGAGGACACCTTGCAAGCTCTGCGACCAATCTCC 163
QY 149 GATGCTGCTCCTGACGCTTCCCTTGAAAGAGGACCCAGACAGCAAGGTTGCTCGCAACA 208
Db 164 GATGCTGCTCCTGACGCTTCCCTTGCAAGAGGACCCAGACAGCAAGGTTGCTCGCAACA 223
QY 209 TGCACCAAGACCAACTTGTGTCATGCTTCGAGAGATCACCAAGGCCAACGTTGAC 268
Db 224 TGCACCAAGACCAACTTGTGTCATGCTTCGAGAGAAATCACGACCAAGGCCAACGTTGAC 283
QY 269 TAGGAGAAGATCGTGGTGCACACCTGCGAGAAACATCGGCTTCGTCTCAACCGATGCGGA 328
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Db 149 GATGCTCTCGACGGCTTCCTCGACGAGACCCGACGCAAGTTGCTCGGAACA 208  
Qy 209 TGCAACCAAGACCACTTGGTCTATGGTCTTCGGAGAGATCACCAACGAGGCAACGTTGAC 268  
Db 209 TGCAACCAACCAACTTGGTCTATGGTCTTCGGAGAAATCACGACCAAGGCAACGTTGAC 268  
Qy 269 TACGAGAGATCGTGGTGACACCTGCAGGAACATCGGCTTCGTCTCAACGATGTGGGA 328  
Db 269 TACGAGAGATAGTGGTGACACCTGCAGGAACATCGGCTTCGTCTCAACGATGTGGGA 328  
Qy 329 CTTGATGCTGACAACTGCAAGTCTCTGTAAACAATTTGAGCAGAGAGCCCTGATATTGCC 388  
Db 329 CTGGATGCCGACAACTGCAAGTCTCTGTCAACAATTTGAGCAGAGAGCCCTGATATTGCT 388  
Qy 389 CAGGGTGTGACGGCCACCTTTACCAAAAGACCGAGGAATCGGTCTGGAGACCAAGGT 448  
Db 389 CAGGGTGTACGGCCACCTTTACCAAAACCTTGAAGAAATTTGGTCTGGTACCAAGGT 448  
Qy 449 CACATGTTGGCTATGCAACGAGCAACCCAGAAATTTGATGCCATTTGATCTATGTTCT 508  
Db 449 CACATGTTGGCTATGCAACGATGAACCCCTGAATTTGATGCCATTTGAGCCATGTTCT 508  
Qy 509 GCAACTAACTCGGTGCTCTCACCGAGTTGCGAAGAACCGAACCTGCCCATGGTTG 568  
Db 509 GCAACAAACTCGGTGCTCTCACCGAGTTGCGAAGAACCGTACCTGCCCTTGGCTG 568  
Qy 569 AGSCCTGATGGGAAACCCCAAGTGTGTTGAGTATTACAATGACACGCTGCCATGGTT 628  
Db 569 AGSCCTGATGGGAAGCCCAAGTGACCGTTGAGTATTACATGACAAATGTTGCCAGGTT 628  
Qy 629 CCAATGCTGTCACACTGTGCTTATCTCCACCAACATGATGAGACTGTGACCAACGAC 688  
Db 629 CCTATTGCTGACACACCGTGTAACTCTCCACCAACGAGAGTGTGACCAATGAC 688  
Qy 689 GAAATGCTGACCTCAAGAGCATGTGATCAAGCCGTGATCCCGAAGAGTACCTT 748  
Db 689 GAAATGCTGACCTCAAGAGCATGTGATCAAGCCGTGATCCCGAAGAGTACCTT 748  
Qy 749 GATGAGAAGACCAATTTTCACTTGAACCCCTCTGGCCGTTTGTCTCAATGGAGTCTCAC 808  
Db 749 GATGAGAAGACCAATTTTCACTTGAACCCCTCTAGCCGTTTGTCTCAATGGGCCCTCAT 808  
Qy 809 GGTGATGCTGGTCTCACCGCCGCAAGATCATCATGATCTTACGGAGGATGGGTGCT 868  
Db 809 GGGATGCTGGTCTCACCGCCGCAAGATCATCATGATCTTATGAGGATGGGTGCT 868  
Qy 869 CATGGTGGTGGTCTTCTCCGGGAAGGATCCCAAGGTTGATAGGAGTGGTCTTAC 928  
Db 869 CATGGTGGTGGTCTTCTCCGGGAAGGACCCCTACCAAGTTGATAGGAGTGGTCTTAC 928  
Qy 929 ATTGTGAGACAGCTGCTAAGACATTTGGCAAGTGGACTAGCCAGAGGTCATTGG 988  
Db 929 ATTGTGAGACAGCTGCTAAGACATTTGGCAAGTGGACTAGCCAGAGGTCATTGG 988  
Qy 989 CAAAGTCTTATGCCATTTGGTGGCCGAGCCCTTGTCTGTCTTGTGACACCTATGGC 1048  
Db 989 CAAAGTCTTATGCCATTTGGTGGCCGAGCCCTTGTCTGTGTTGTGACACCTATGGC 1048  
Qy 1049 ACCGGGAAGATCATGATAGGAGATTTCAACATTTGTGAAGAGAACTTTGATTTGAG 1108  
Db 1049 ACTGGGAAGATCATGATAGGAGATTTCAACATTTGTGAAGGAACCTTTGATTTGAG 1108  
Qy 1109 CCGGATGATGCTCCATCAACCTTTGATCTCAAGAGGGTGGGAATAACAGGTTCTTGAAG 1168  
Db 1109 CCGGATGATGCTCCATCAACCTTTGATCTCAAGAGGGTGGGAATAACAGGTTTGAAG 1168  
Qy 1169 ACTGCTGCATATGGACACTTCCGAGAGAGGACCTTGACTTCAATGGGAAGTGGTCAAG 1228  
Db 1169 ACTGCTGCATATGGACACTTGGGAAGAGACCTTGACTTCAATGGGAAGTGGTCAAA 1228  
Qy 1229 CCCTCAAGTGGGAGAGCCCTTAAGGCCATTTCAATCCATGTCATGTCGAGGATTTT 1288

Db 1229 CCCCTCAAGTGGGAGAGGCCCTAA-GTAATTCATTCACCTGCTATAGTGGGAAGTTTT 1287  
Qy 1289 T-AGCGTTGCCCTTATA--ATGCTATTATCCATACTTTCCACGTCCTTGTCTGTGT 1345  
Db 1288 TGAGCGTTGCCCTTATAATATGCTTAATATCCATACTTTCCACGTCCTTACTCTGTGT 1347  
Qy 1346 TTTTCTCTCGTCTCTCTCTCTATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1405  
Db 1348 GTTCT 1403  
Qy 1406 ATGATCACTAAATAA-ATGCTACTCTCTGTTT-----TCCGACCAATGCTCTCTTA 1455  
Db 1404 GTGATCACTAAATAAATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTTA 1463  
Qy 1456 ATATCAGTATCAAAAAGAAATGT 1477  
Db 1464 ATATCAATATCAAAAAGAGAGT 1485

RESULT 12  
US-10-425-114-11712  
; Sequence 11712, Application US/10425114  
; Publication No. US2004003488A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 11712  
; LENGTH: 1505  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 701123183\_FLI  
US-10-425-114-11712

Query Match 81.1%; Score 1204.4; DB 18; Length 1505;  
Best Local Similarity 91.9%; Pred. No. 0;  
Matches 1343; Conservative 0; Mismatches 101; Indels 18; Gaps 6;

Qy 29 CT 88  
Db 40 CCCTTTCTGCT 99  
Qy 89 CTATTACTCTAGATCTAGTGAACGAGGACACCTTGACAACTCTGACAACTCTGCAACCAATCTCC 148  
Db 100 CTATTACTCTAGATCTAGTGAACGAGGACACCTTGACAACTCTGCAACCAATCTCTCC 159  
Qy 149 GATGCTGCTCTCGACGCTTTCCTTCAACAGGACCCAGACAGCAAGTTCCTCGCAACA 208  
Db 160 GATGCTGCTCTCGACGCTTTCCTTCAACAGGACCCAGACAGCAAGTTCCTCGCAACA 219  
Qy 209 TGCACCAAGACCAACTTGGTCTATGCTCTTCCGAGAGATCACCAAGCCCAACGTTGAC 268  
Db 220 TGCACCAAAACCAACTTGGTCTATGCTCTTCCGAGAAATTCACGACCAAGCCCAACGTTGAC 279  
Qy 269 TACGAGAAGATCGTGGTGACACCTTGACAGGAAATCGGCTTCTCTCAACCAATGAGGGA 328  
Db 280 TACGAGAAGATAGTGGTGACACCTTGACAGGAAATCGGCTTCTCTCAATGATGAGGGA 339  
Qy 329 CTTGATGCTGACAACTGCAAGGTCCTTGTAAACATTTGAGCAGCAGAGCCCTGATATTGCC 388  
Db 340 CTTGATGCGGACAACTGCAAGGTCCTTGTCAACATTTGAGCAGCAGAGCCCTGATATTGCT 399  
Qy 389 CAGGGTGTGCAACGGCCACTTACCAAAAGACCCGAGGAATCGGTGCTGGAGACCGGAT 448







Db 645 CCTATTGCTGACACCGTGTCTAAATCTCCACCAACACACGAGACTGTCCACATGAC 704  
QY 689 GAAATTCGAGCTGACCTCAAGGAGCATGTGATCAAGCCGGTGTATCCCGGAGAGTACCTTT 748  
Db 705 GAAATTCGCTGCTGACCTCAAAGAGCATGTGATCAAGCCTGTGATCCACGAGAGTACCTT 764  
QY 749 GATGAGAGACCAATTTTCACCTTGAACCCCTCTGGCGGTTTTTGTCTCATTTGAGAGTCTCTAC 808  
Db 765 GATGAGAGACCAATTTTCACCTTGAACCCCTCTAGGCCGTTTTTGTCTCATTTGCTGGCCCTCAT 824  
QY 809 GGTGATGCTGTCTCACCGCCGCAAGATCATCATCGATCTTACCGAGGATGGGGTGT 868  
Db 825 GGGCATGCTGTCTCACCGCCGCAAGATCATTTATCGATCTTATGAGAGATGGGGTGT 884  
QY 869 CATGGTGGTGGTCTTCTCCGGGAAGGATCCACCAAGGTTGATAGGAGTGGTCTTAC 928  
Db 885 CATGGTGGTGGTCTTCTCCGGGAAGGATCCACCAAGTGTGATAGGAGTGGTCTTAC 944  
QY 929 ATGTGAGACAGCTGCTAAGAGCATTTGGGCAAGTGGACTAGCCAGAAAGGTGCATTTG 988  
Db 945 ATGTGAGACAGCTGCTAAGAGCATTTGGGCAAGTGGACTTGCACCAAGGTGCATTTG 1004  
QY 989 CAAAGTCTTATGCCATTTGGTGGCCGAGCCCTTCTGTCTTGTCTTGTCTGACACCTATG 1048  
Db 1005 CAAAGTCTTATGCCATTTGGTGGCCGAGCCCTTCTGTCTTGTCTTGTCTGACACCTATG 1064  
QY 1049 ACCGGGAAGATCCATGATGAAGAGATTCTCAACATTTGGAAGGAACTTTGATTTGAG 1108  
Db 1065 ACTGGGAAGATCCATGATGAAGAGATTCTCAACATTTGGAAGGAACTTTGATTTGAG 1124  
QY 1109 CCGGTTATGATCTCCATCAACCTTGATCTCAAGAGGGGTGGGAATTAACAGGTTCTTGAAG 1168  
Db 1125 CCGGTTATGATCTCCATCAACCTTGATCTCAAGAGGGGTGGGAATTAACAGGTTCTTGAAG 1184  
QY 1169 ACTGCTGATATGGACATCTGGCAGAGAGGACCTGATCTCAATGGAAGTGTCTGAC 1228  
Db 1185 ACTGCTGATATGGACATCTGGCAGAGAGGACCTGATCTCAATGGAAGTGTCTGAC 1244  
QY 1229 CCGCTCAAGTGGGAGAGGCTTAAGGCCATTCAATTCATCTGCAATGTGCTGGAGTTTTT 1288  
Db 1245 CCGCTCAAGTGGGAGAGGCTTAAGGCCATTCAATTCATCTGCAATGTGCTGGAGTTTTT 1303  
QY 1289 T-AGGCTTCCCTTATA--ATGCTATATTCATAACTTTCAAGCCCTTCTGCTGTGT 1345  
Db 1304 TGAGCGTTCCCTTATAATATGCTAATATCCATTAATTTCAAGCTCTCTTACTCTGTGT 1363  
QY 1346 TTTTCTCTGCTGCTCCTCTATTTTGTCTCTGCTCTTCTTCTTCTTCTTCTTCTTCTTCT 1405  
Db 1364 GTTCT 1419  
QY 1406 ATGATCAACTAAAAA-ATGCTACTCTCTGTTT-----TCCGACCATTTGTCTCTTA 1455  
Db 1420 GTGATCAACTAAAAAATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1479  
QY 1456 ATATCAAGTATCAAAAAAGATGT 1477  
Db 1480 ATATCAATATCAAAAAAGAGAT 1501

## RESULT 14

US-10-425-114-8323  
; Sequence 8323, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E.  
; APPLICANT: Tabaska, Jack E.  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; NUMBER FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 8323  
; LENGTH: 1514  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700747484\_FLI  
US-10-425-114-8323

Query Match 81.1%; Score 1204.4; DB 18; Length 1514;  
Best Local Similarity 91.9%; Pred. No. 0;  
Matches 1343; Conservative 0; Mismatches 101; Indels 18; Gaps 6;

QY 29 CTCTCTCTGCTCTCTCTTCTTACCTTTCAAGTTTTTAAAGATTAAAGATGCGAGAGACATTC 88  
Db 49 CCTCTTCTGCTCTCTCTTCTTACCTTTCAAGTTTTTAAAGATTAAAGATGCGAGAGACATTC 108  
QY 89 CTATTTACCTCAGAGTCAAGTGAACGAGGAGACACCTTGACAAGCTCTGCGACCAAAATCTCC 148  
Db 109 CTATTTACCTCAGAGTCAAGTGAACGAGGAGACACCTTGACAAGCTCTGCGACCAAAATCTCC 168  
QY 149 GATGCTGTCTCGACGCTTGCCTTGAACAGGACCCAGACAGCAAGTTCCTGCGGAAACA 208  
Db 169 GATGCTGTCTCGACGCTTGCCTTGAACAGGACCCAGACAGCAAGTTCCTGCGGAAACA 228  
QY 209 TGCACCAAGACCAACTTGGTCTATGCTTTCGAGAGATCACCACCAAGGCCAACGTTGAC 268  
Db 229 TGCACCAAAACCACTTGGTCTATGCTTTCGAGAGAAATCACCACCAAGGCCAACGTTGAC 288  
QY 269 TACGAGAAAGATCGTCTGCTGACACCTGCGAGGAACATCGGCTTCTCTCAACGATGTGGGA 328  
Db 289 TACGAGAAAGATAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 348  
QY 329 TTGTATGTGCAACATGCAAGTCTCTTGAACATTTGAGAGAGAGAGAGAGAGAGAGAGAG 388  
Db 349 CTGATGCGGACAACTGCAAGGCTCTCTGCAAAATTTGAGAGAGAGAGAGAGAGAGAGAG 408  
QY 389 CAGGGTGTGCAAGGACCTTACCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 448  
Db 409 CAGGGTGTGCAAGGACCTTACCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 468  
QY 449 CACATGTTTGGTATGCGACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 508  
Db 469 CACATGTTTGGTATGCGACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 528  
QY 509 GCAACTAAATCTGCTGCTCTCAAGAGGTTGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 568  
Db 529 GCAACAAATCTGCTGCTCTCAAGAGGTTGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 588  
QY 569 AGGCTGTATGGAG 628  
Db 589 AGGCTGTATGGAG 648  
QY 629 CCAGTTCGTGTCCACATGCTTATCTCCACCCCAACATGATGAGAGAGAGAGAGAGAGAGAG 688  
Db 649 CCTATTCTGTATACACACCGTGTCTATCTCCACCCCAACAGAGAGAGAGAGAGAGAGAGAG 708  
QY 689 GAAATTCAGCTGACCTCAAG 748  
Db 709 GAAATTCAGCTGACCTCAAG 768  
QY 749 GATGAG 808  
Db 769 GATGAG 828  
QY 809 GGTGATGCTGTCTCTACCGGCGGCAAGATCATCATCGATCTTACCGGAGAGAGAGAGAGAGAG 868  
Db 829 GGCATGCTGTCTCTACCGGCGGCAAGATCATCATCGATCTTACCGGAGAGAGAGAGAGAGAG 888  
QY 869 CATGCTGTGTGTCTTCTCCGGGAAGAGATCCCAAGGTTGATAGAGAGAGAGAGAGAGAGAG 928





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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: August 25, 2005, 16:54:06 ; Search time 226 Seconds  
(without alignments)  
5082.647 Million cell updates/sec

Title: US-10-734-698A-38  
Perfect score: 2748  
Sequence: 1 AGCCAGAGCCCACTCAACCA.....CAAAGAATGTTCCAAATT 1485

Scoring table: BLOSUM62 Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 2105692 seqs, 386760381 residues  
Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ n2p.model -DBV=xlp  
-Q=/cpn2.1/USPTO.spool\_p/US10734698/runat\_25082005\_105359\_10255/app\_query.fasta\_1.1671  
-DB=A\_Geneseq -QMT=fastcan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdd -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10734698 @CGN 1.1 236 @runat\_25082005\_105359\_10255 -NCPU=6 -ICPU=3  
-NO WMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A\_Geneseq\_16Dec04:\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001s:\*  
5: Geneseq2002s:\*  
6: Geneseq2003as:\*  
7: Geneseq2003ba:\*  
8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2083	75.8	392	2	Aaw97743 Soybean S
2	1947	70.9	393	3	Aag40366 Arabidops
3	1946	70.8	396	2	Aaw97742 Corn S-ad
4	1940	70.6	393	3	Aag06584 Arabidops
5	1935	70.4	393	3	Aag07760 Arabidops
6	1935	70.4	393	3	Aag37871 Arabidops
7	1900.5	69.2	392	3	Aag43921 Zea mays
8	1900.5	69.2	394	2	Aaw34542 S-adenosy
9	1900.5	69.2	394	2	Aaw34540 S-adenosy
10	1891.5	68.8	394	2	Aaw97744 Wheat S-a

11	1886.5	68.6	394	2	Aaw34541 S-adenosy
12	1878.5	68.4	439	3	Aag39107 Arabidops
13	1872	68.1	390	3	Aag39108 Arabidops
14	1869	68.0	390	4	Aay72078 Nicotiana
15	1688	61.4	344	3	Aag40367 Arabidops
16	1685	61.3	344	3	Aag37872 Arabidops
17	1685	61.3	344	3	Aag07761 Arabidops
18	1682	61.2	342	3	Aag40368 Arabidops
19	1681	61.2	344	3	Aag06585 Arabidops
20	1679	61.1	342	3	Aag07762 Arabidops
21	1679	61.1	342	3	Aag37873 Arabidops
22	1675	61.0	342	3	Aag06586 Arabidops
23	1648.5	60.0	341	3	Aag43922 Zea mays
24	1642.5	59.8	339	3	Aag43923 Zea mays
25	1632	59.4	368	3	Aag06943 Arabidops
26	1631	59.4	364	3	Aag06944 Arabidops
27	1618	58.9	341	3	Aag39109 Arabidops
28	1501	54.6	311	3	Aag06945 Arabidops
29	1427	51.9	281	7	Abm73962 DNA clone
30	1422	51.7	279	7	Abm73650 DNA clone
31	1316.5	47.9	395	8	ADL12742 Human ste
32	1316.5	47.9	395	8	ADJ75310 Marker ge
33	1316.5	47.9	395	8	AD019099 Human PRO
34	1316.5	47.9	395	8	AD019097 Human PRO
35	1316.5	47.9	395	8	ADQ91618 Human met
36	1316.5	47.9	395	8	ABM80322 Tumour-as
37	1278.5	46.5	395	8	ADs17324 Rat liver
38	1274.5	46.4	382	8	ADs44164 Bacterial
39	1274.5	46.4	395	6	ABO07244 Human p53
40	1274.5	46.4	395	7	ADD48234 Human Pro
41	1274.5	46.4	395	8	ADQ88198 Human 730
42	1268	46.1	397	7	ADD48232 Rat Prote
43	1262.5	45.9	385	3	Aay95075 Candida a
44	1259.5	45.8	424	8	ADP04591 Sea squir
45	1243.5	45.3	398	4	ABg22853 Novel hum

ALIGNMENTS

RESULT 1  
Aaw97743  
ID Aaw97743 standard; protein; 392 AA.  
XX  
AC Aaw97743;  
XX  
DT 21-MAY-1999 (first entry)  
XX  
DE Soybean S-adenosylmethionine synthetase.  
XX

XX  
KW S-Adenosylmethionine synthetase; soybean; amino acid; lysine; threonine; methionine; cysteine; isoleucine; transgenic plant; crop improvement; food; feedstuff.  
XX  
OS Glycine max.  
XX  
PN WO9855601-A2.  
XX  
PD 10-DEC-1998.  
XX  
PF 05-JUN-1998; 98WO-US011692.  
XX  
PR 06-JUN-1997; 97US-0048771P.  
PR 12-JUN-1997; 97US-0049443P.  
XX  
(DUPO) DU PONT DE NEMOURS & CO E I.  
PA Falco SC, Allen SM, Rafalski JA, Hitz WD, Kinney AJ, Abell LM;  
PI Thorpe CJ;  
XX WPI: 1999-070263/06.  
DR N-PSDB; AAX07184.  
XX  
PT New plant amino acid biosynthetic enzymes, DNA and chimeric genes -

PT encode: dihydropicolinate reductase; diaminopimelate epimerase; threonine  
 PT synthase; threonine deaminase; S-adenosylmethionine synthetase.  
 XX Example 7; Page 67-68; 98pp; English.

XX This is the amino acid sequence of a full-length soybean S-  
 CC adenosylmethionine synthetase, as deduced from a cDNA clone (see  
 CC AAX07184), designated s2.12b06, obtained from a soybean seed cDNA  
 CC library. The soybean enzyme shows sequence similarity to the tomato  
 CC enzyme. The invention relates to new isolated nucleic acid fragments (see  
 CC AAX07166-85) encoding plant enzymes (see AAW97727-44) that catalyze steps  
 CC in the biosynthesis of lysine, threonine, methionine, cysteine and  
 CC isoleucine from aspartate, the enzyme being selected from  
 CC dihydropicolinate reductase, diaminopimelate epimerase, threonine  
 CC synthase, threonine deaminase or S-adenosylmethionine synthetase. The  
 CC invention also relates to the construction of a chimeric gene encoding  
 CC all or a portion of the biosynthetic pathway enzyme, in sense or  
 CC antisense orientation, where expression of the chimeric gene results in  
 CC production of altered levels of the enzyme in a transformed host cell.  
 CC Overexpression or reduction of expression of genes encoding the amino  
 CC acid biosynthetic pathway enzymes in crop plants such as corn, soybean  
 CC and wheat can be used to alter levels of the amino acids in human food  
 CC and animal feed. Transformed host cells can also be used to identify  
 CC compounds that inhibit one of the enzymes

XX Sequence 392 AA;

#### Alignment Scores:

Pred. No.: 6.19e-201 Length: 392  
 Score: 2083.00 Matches: 392  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 75.80% Indels: 0  
 DB: 2 Gaps: 0

US-10-734-698A-38 (1-1485) x AAW97743 (1-392)

QY 74 ATGGGAGACATCTCTATTACCTCAGATCAGTGAAGGAGACACCTCAGAGCTC 133  
 Db 1 MetAlaGluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeu 20  
 QY 134 TGGCACCAATCTCCGATGCTGCTCGACGGCTTGCCTTGAACAGGACCCAGACGCAAG 193  
 Db 21 CysAspGlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLys 40  
 QY 194 GTTGCTCGCAACATGCAACAGCAACCTTGCTCATGGTCTTCGAGAGATCACACC 253  
 Db 41 ValAlaCysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThr 60  
 QY 254 AAGGCCAAGTTGACTACGAGAGATCGTCGCTGACACCTCGAGGACATCGGCTCGTC 313  
 Db 61 LysAlaAsnValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheVal 80  
 QY 314 TCAACGATGTGGACTGTGCTGCACTGCACTGCAAGTCTTGTAAACATTGACAGAGAG 373  
 Db 81 SerAsnAspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGln 100  
 QY 374 AGCCCTGATATTGCCCGGCTGTGACCGCCACCTTACCAAGACCCGAGGAATTCGGT 433  
 Db 101 SerProAspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGly 120  
 QY 434 GCTGGAGACAGGGTACATGTTGGCTATGCCAGGAGAAACCCAGAAATTGATGCCA 493  
 Db 121 AlaGlyAspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetPro 140  
 QY 494 TTGAGTCATGTTCTTCAACTAACTCGGTGCTCGTCTCACCGAGGTTCGCAAGAACGGA 553  
 Db 141 LeuSerHisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGly 160  
 QY 554 ACTGCCCATGTTGAGGCTGATGGGAAACCCAAAGTCACTGTTGAGTATTCAATGAC 613  
 Db 161 ThrCysProThrLeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnAsp 180

QY 614 AACGGTGCCATGGTTCCAGTTCTGTCACACTGTGCTTATCTCCACCCCAACATGATGAG 673  
 Db 181 AsnGlyAlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGlu 200  
 QY 674 ACTGTGACCAACGACGAAATTCGACGTGACCTCAAGGAGCATGTGATCAAGCCCGTGTATC 733  
 Db 201 ThrValThrAsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIle 220  
 QY 734 CCGAGAAAGTACCTTGATGAGAAGACCACTTTTCCACTTGAAACCCCTCTGGCGGTTTGTTC 793  
 Db 221 ProGluLysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheVal 240  
 QY 794 ATTGAGGTCTCTCAGGGTGATGCTGCTCACCGCCGCAAGATCATCATCGATACTTAC 853  
 Db 241 IleGlyGlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleIleAspThrTyr 260  
 QY 854 GGAGATGGGTGCTCATGTGGTGGTGGTCTTCTCCGGGAAGGATCCCAAGGTTGAT 913  
 Db 261 GlyGlyTyrGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAsp 280  
 QY 914 AGGAGTGTGCTTACATTGTGAGACAGCTGCTTAAGACATTTGGCAAGTGGACTAGCC 973  
 Db 281 ArgSerGlyAlaTyrIleValArgGlnAlaAlaLysSerIleValAlaSerGlyLeuAla 300  
 QY 974 AGAAGTGCATTGTGCAAGTGTCTTATGCCATTGTGTGCCGAGCCCTTGTCTGCTTT 1033  
 Db 301 ArgArgCysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPhe 320  
 QY 1034 GTTGACACTATGGCACCGGGAAGATCCATGATGAAGAGATTCTCAACATTGTGAAGAG 1093  
 Db 321 ValAspThrTyrGlyThrGlyLysIleHisAspLysGluIleLeuAsnIleValLysGlu 340  
 QY 1094 AACTTTGATTTCCAGCCCGGTATGATCTCCATCAACCTTGATCTCAAGAGGGTGGGAAT 1153  
 Db 341 AsnPheAspPheArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyGlyAsn 360  
 QY 1154 AACAGGTTCTTGAAGACTGCTGCATATGACACATTCGGCAGAGAGACCCCTGACTTCACA 1213  
 Db 361 AsnArgPheLeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThr 380  
 QY 1214 TGGGAAGTGGTCAAGCCCTCAAGTGGGAGAGGCC 1249  
 Db 381 TrpGluValValLysProLeuLysTrpGluLysAla 392

RESULT 2  
 AAG40366  
 ID AAG40366 standard; protein; 393 AA.  
 XX AAG40366;  
 XX 18-OCT-2000 (first entry)  
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KW threonine; methionine; cysteine; isoleucine; transgenic plant;
KW crop improvement; food; feedstuff.
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PR 22-SEP-1999; 99US-0155139P.  
PR 23-SEP-1999; 99US-0155486P.  
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PR 28-SEP-1999; 99US-0156458P.



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PR 04-OCT-1999;	99US-0157117P.	1935.00			
PR 05-OCT-1999;	99US-0157753P.	97.17%			
PR 06-OCT-1999;	99US-0157865P.	93.32%			
PR 07-OCT-1999;	99US-0158029P.	70.41%			
PR 08-OCT-1999;	99US-0158232P.	3			
PR 12-OCT-1999;	99US-0158369P.				
PR 13-OCT-1999;	99US-0159239P.				
PR 13-OCT-1999;	99US-0159294P.				
PR 13-OCT-1999;	99US-0159295P.				
PR 14-OCT-1999;	99US-0159330P.				
PR 14-OCT-1999;	99US-0159331P.				
PR 14-OCT-1999;	99US-0159637P.				
PR 14-OCT-1999;	99US-0159638P.				
PR 18-OCT-1999;	99US-0159584P.				
PR 21-OCT-1999;	99US-0160741P.				
PR 21-OCT-1999;	99US-0160767P.				
PR 21-OCT-1999;	99US-0160768P.				
PR 21-OCT-1999;	99US-0160770P.				
PR 21-OCT-1999;	99US-0160814P.				
PR 21-OCT-1999;	99US-0160815P.				
PR 22-OCT-1999;	99US-0160980P.				
PR 22-OCT-1999;	99US-0160981P.				
PR 22-OCT-1999;	99US-0160989P.				
PR 25-OCT-1999;	99US-0161404P.				
PR 25-OCT-1999;	99US-0161405P.				
PR 25-OCT-1999;	99US-0161406P.				
PR 26-OCT-1999;	99US-0161359P.				
PR 26-OCT-1999;	99US-0161360P.				
PR 26-OCT-1999;	99US-0161361P.				
PR 28-OCT-1999;	99US-0161920P.				
PR 28-OCT-1999;	99US-0161992P.				
PR 28-OCT-1999;	99US-0161993P.				
PR 29-OCT-1999;	99US-0162142P.				

Alignment Scores:

Pred. No.: 5.76e-186 Length: 393

Score: 1935.00 Matches: 363

Percent Similarity: 97.17% Conservative: 15

Best Local Similarity: 93.32% Mismatches: 11

Query Match: 70.41% Indels: 0

DB: 3 Gaps: 0

US-10-734-698A-38 (1-1485) x AAG37871 (1-393)

QY	80	GAGACATTCCTATTTACCTCAGAGTCAGTGAACGAGGGACACCTGACAAGCTCTCGAC	139
DB	2	GlusSerPheLeuPheThrSerGluSerValAenGluGlyHisProAspLysLeuCysAsp	21
QY	140	CAAAATCTCGGATGCTGCTCTCGACGCTTGCTTGAACAGGACCCAGACAGCAAGGTTCGC	199
DB	22	GlnIleSerAspAlaIleLeuAspAlaCysLeuGluGlnAspProGluSerLysValAla	41
QY	200	TGCGAAACATGCAACCAAGACCAACTTGCTTGCTCATGGTCTTCGGAGAGATCACCAAGGCC	259
DB	42	CysGluThrCysThrLysThrAsnMetValMetValPheGlyGluIleThrThrLysAla	61
QY	260	AAGCTTGACTACGAGAGAGATCGTGGTGACACCTGCGAGGAACATCGGCTTCGTCTCAAC	319
DB	62	AsnValAspTyrGluGlnIleValArgLysThrCysArgGluIleGlyPheValSerAla	81
QY	320	GATGTGGACTTGATGCTGCAACATGCAAGTTCCTTGTAAACATTGAGCAGACAGCCCT	379
DB	82	AspValIleGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGlnGlnSerPro	101
QY	380	GATATTGCCAGGGTGTGCAACGGCCACCTTACCAAAAAGACCCGAGGAAATTCGGTGTGGA	439
DB	102	AspIleAlaGlnGlyValHisGlyHisLeuThrLysLysProGluGluValGlyAlaGly	121
QY	440	GACCAAGGTTCATGTTTGGCTATGCCACGACGAAACCCGAGAAATTCATTCATTCAGT	499
DB	122	AspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuThr	141

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PR	05-MAR-1999;	99US-0123180P.	99US-0142977P.
PR	09-MAR-1999;	99US-0123548P.	99US-0143542P.
PR	23-MAR-1999;	99US-0125788P.	99US-0143624P.
PR	25-MAR-1999;	99US-0126264P.	99US-0144005P.
PR	29-MAR-1999;	99US-0126785P.	99US-0144085P.
PR	01-APR-1999;	99US-0127462P.	99US-0144086P.
PR	06-APR-1999;	99US-0128234P.	99US-0144325P.
PR	08-APR-1999;	99US-0128714P.	99US-0144331P.
PR	16-APR-1999;	99US-0129845P.	99US-0144333P.
PR	19-APR-1999;	99US-0130077P.	99US-0144334P.
PR	21-APR-1999;	99US-0130449P.	99US-0144335P.
PR	23-APR-1999;	99US-0130510P.	99US-0144352P.
PR	23-APR-1999;	99US-0130891P.	99US-0144632P.
PR	28-APR-1999;	99US-0131449P.	99US-0144884P.
PR	30-APR-1999;	99US-0132048P.	99US-0144814P.
PR	30-APR-1999;	99US-0132407P.	99US-0145086P.
PR	04-MAY-1999;	99US-0132484P.	99US-0145088P.
PR	05-MAY-1999;	99US-0132485P.	99US-0145085P.
PR	06-MAY-1999;	99US-0132486P.	99US-0145087P.
PR	06-MAY-1999;	99US-0132487P.	99US-0145089P.
PR	07-MAY-1999;	99US-0132863P.	99US-0145192P.
PR	11-MAY-1999;	99US-0134256P.	99US-0145145P.
PR	14-MAY-1999;	99US-0134218P.	99US-0145218P.
PR	14-MAY-1999;	99US-0134219P.	99US-0145224P.
PR	14-MAY-1999;	99US-0134221P.	99US-0145276P.
PR	14-MAY-1999;	99US-0134370P.	99US-0145913P.
PR	18-MAY-1999;	99US-0134376P.	99US-0145918P.
PR	19-MAY-1999;	99US-0134941P.	99US-0145919P.
PR	20-MAY-1999;	99US-0135124P.	99US-0145951P.
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PR	10-JUN-1999;	99US-0138540P.	99US-0147493P.
PR	10-JUN-1999;	99US-0138847P.	99US-0147935P.
PR	14-JUN-1999;	99US-0139119P.	99US-0148171P.
PR	16-JUN-1999;	99US-0139452P.	99US-0148319P.
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PR	18-JUN-1999;	99US-0139457P.	99US-0149426P.
PR	18-JUN-1999;	99US-0139458P.	99US-0149722P.
PR	18-JUN-1999;	99US-0139459P.	99US-0149723P.
PR	18-JUN-1999;	99US-0139460P.	99US-0149929P.
PR	18-JUN-1999;	99US-0139461P.	99US-0149902P.
PR	18-JUN-1999;	99US-0139462P.	99US-0149930P.
PR	18-JUN-1999;	99US-0139463P.	99US-0150566P.
PR	18-JUN-1999;	99US-0139457P.	99US-0150884P.
PR	18-JUN-1999;	99US-0139763P.	99US-0151065P.
PR	21-JUN-1999;	99US-0139817P.	99US-0151066P.
PR	22-JUN-1999;	99US-0139899P.	99US-0151080P.
PR	23-JUN-1999;	99US-0140353P.	99US-0151303P.
PR	23-JUN-1999;	99US-0140354P.	99US-0151438P.
PR	24-JUN-1999;	99US-0140695P.	99US-0151930P.
PR	28-JUN-1999;	99US-0140823P.	99US-0152363P.
PR	29-JUN-1999;	99US-0140591P.	99US-0153070P.
PR	30-JUN-1999;	99US-0141287P.	99US-0153758P.
PR	01-JUL-1999;	99US-0141842P.	99US-0154018P.
PR	01-JUL-1999;	99US-0142154P.	99US-0154039P.
PR	02-JUL-1999;	99US-0142055P.	99US-0154779P.
PR	06-JUL-1999;	99US-0142390P.	99US-0155139P.
PR	08-JUL-1999;	99US-0142803P.	99US-0155486P.
PR			99US-0155659P.



XX 28-MAY-1996; 96JP-00133406.  
 XX (NIOC ) NIPPON OIL CO LTD.  
 XX WPI; 1998-080077/08.  
 XX N-PSDB; AAT99143.  
 XX S-adenosyl-methionine synthase gene - useful in producing plants  
 PT resistant to alkaline soil.  
 XX Claim 3; Page 7-8; 13pp; Japanese.  
 XX This sequence represents the S-adenosylmethionine synthase 3 (sam3)  
 CC protein. The DNA encoding this sequence may be used in producing plants  
 CC which are resistant to alkaline soil  
 XX Sequence 394 AA;  
 SQ

Alignment Scores:  
 Pred. No.: 1,78e-182 Length: 394  
 Score: 1900.50 Matches: 354  
 Percent Similarity: 96.16% Conservative: 22  
 Best Local Similarity: 90.54% Mismatches: 14  
 Query Match: 69.16% Indels: 1  
 DB: 2 Gaps: 1

US-10-734-698A-38 (1-1485) x AAW34542 (1-394)

QY 77 GCAGAGACATTCCTATTTACCTCAGAGTCAGTGAACGAGGACACCCCTGACAGCTCTGC 136  
 Db 3 AlaGluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCyB 22

QY 137 GACCAAAATCTCGATGCTGCTCTGACGCTTGGCTTGAACAGAGCCGACAGACGAGTT 196  
 Db 23 AspGlnValSerAspAlaValLeuAspAlaCysLeuAlaGlnAspProAspSerLysVal 42

QY 197 GCTCGGAACATGCACCAAGACCACTTGGTCATGGTCTTCGGAGAGATCACCCACAG 256  
 Db 43 AlaCysGluThrCysThrLysThrAsnMetValMetValPheGlyGluThrThrLys 62

QY 257 GCCAAGCTTGACTACGAGAGATCGTGCCTGACACCTCGAGGAACATCGCTCTCA 316  
 Db 63 AlaThrValAspTyrGluLysLeuValArgAspThrCysArgAspIleGlyPheIleSer 82

QY 317 AACGATGGGACTTGATCTGACAACTGCAAGTCTCTTGTAAACATTCAGCAGCAGAC 376  
 Db 83 AspAspValGlyLeuAspAlaAspHisCysLysValLeuValAsnIleGluGlnSer 102

QY 377 CCTGATATTGCCAGGCTGTCACGGCCACCTTACCAGGAGACCCGAGGAATCGTGTCT 436  
 Db 103 ProAspIleAlaGlnGlyValHisGlyHisPheThrLysArgProGluValGlyAla 122

QY 437 GGAGACAGGGTCACATGTTGGCTATGCGCAGGACGAAACCCAGAAATTCATGTCATTG 496  
 Db 123 GlyAspGlnGlyLeuMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeu 142

QY 497 AGTCATGTTCTTGCAACTAACTCGGTGCTGCTCACCAGGTTTCGCAAGAACGGAACC 556  
 Db 143 ThrHisMetLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThr 162

QY 557 TGCCTCATGTTGAGGCTCATGGGAACCCAGTGACTGTTGAGTATTCATACATGACAC 616  
 Db 163 CysAlaThrLeuArgProAspGlyLysThrGlnValThrIleGluThrLeuAsnGluGly 182

QY 617 GTTGCCATGTTCCAGTTCGTGTCACACTGTGCTTATCTCCACCCCAACATGATGAGCT 676  
 Db 183 GlyAlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGluThr 202

QY 677 GTGACCAACGACGAAATTCAGCTGACCTCAGGAGCATGTGATCAAGCCGGTGTCCCG 736  
 Db 203 ValThrAsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIlePro 222

QY 737 GAGAAGTACCTTGATGAGAGACACCATTTTCCACTTGAACCCCTCTGGCCGTTTGTCTATT 796  
 Db 223 GlyLysTyrLeuAspGluAsnThrIlePheHisLeuAsnProSerGlyArgPheValIle 242

QY 797 GGAGGTCCTCAGGTGATGCTGGTCTACCCGGCCGCAAGATCATCATCTTACCGGA 856  
 Db 243 GlyGlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyrGly 262

QY 857 GGATGGGTGCTCATGTTGGTGGTCTTCTCCGGGAAGGATCCACCACCAAGTTGATAGG 916  
 Db 263 GlyTrpGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArg 282

QY 917 AGTGGTCTTACATTGTGACAGCAGGCTGCTAAGAGCATTGTGGCAAGTGGACTAGCCAGA 976  
 Db 283 SerGlyAlaTyrIleAlaArgGlnAlaAlaLysSerIleIleAlaSerGlyLeuAlaArg 302

QY 977 AGTGCAATGTGCAAGTGTCTTATGCCATTGGTGTGCCGAGCCCTTGTCTGTCTTTGTT 1036  
 Db 303 ArgCysIleValGlnIleSerTyrAlaIleGlyValProGluProLeuSerValPheVal 322

QY 1037 GACACCTATGCGACCGGGAAGATCCATGATAAGAGATTCTCAACATTGTGAAGGAGAAC 1096  
 Db 323 AspSerTyrGlyThrGlyLysIleProAspArgGluIleLeuLysLeuValLysGluAsn 342

QY 1097 TTTGATTTTCAGGCCCGGTATGATCTCCATCAACCTTGATCTCAAGAGGGGTGGGAATAAC 1156  
 Db 343 PheAspPheArgProGlyMetIleThrIleAsnLeuAspLeuLysGlyGly--Lys 361

QY 1157 AGGTTCTTGAAGACTGTGCTGATATGGACATCTTCGAGAGAGGACCCCTGATTCACATGG 1216  
 Db 362 ArgPheIleLysThrAlaAlaTyrGlyHisPheGlyArgAspAlaAspPheThrTrp 381

QY 1217 GAAGTGGTCAAGCCCTCAAGTGGGAGAGGCC 1249  
 Db 382 GluValValLysProLeuLysPheAspLysAla 392

RESULT 9  
 AAW34540  
 ID AAW34540 standard; protein; 394 AA.  
 XX AC AAW34540;  
 XX DT 26-MAR-1998 (first entry)  
 XX DE S-adenosylmethionine synthase 1.  
 XX KW S-adenosylmethionine synthase 1; sam1; barley; alkali resistant plant.  
 XX OS Hordeum vulgare.  
 XX PN JP093113186-A.  
 XX PD 09-DEC-1997.  
 XX PF 28-MAY-1996; 96JP-00133406.  
 XX PR 28-MAY-1996; 96JP-00133406.  
 XX PA (NIOC ) NIPPON OIL CO LTD.  
 XX DR WPI; 1998-080077/08.  
 XX N-PSDB; AAT99141.  
 XX S-adenosyl-methionine synthase gene - useful in producing plants  
 PT resistant to alkaline soil.  
 XX Claim 1; Page 5-6; 13pp; Japanese.  
 XX CC This sequence represents the S-adenosylmethionine synthase 1 (sam1)  
 CC protein. The DNA encoding this sequence may be used in producing plants  
 CC which are resistant to alkaline soil  
 XX Sequence 394 AA;

Alignment Scores:

Pred. No.: 1.78e-182 Length: 394  
Score: 1900.50 Matches: 354  
Percent Similarity: 96.16% Conservative: 22  
Best Local Similarity: 90.54% Mismatches: 14  
Query Match: 69.16% Indels: 1  
DB: 2 Gaps: 1

US-10-734-698A-38 (1-1485) x AAW34540 (1-394)

QY	77	GCAGAGACATTCCTATTACCTCAGAGTCAAGAGGACACCTGACAGCTCTGC	136
DB	3	AlaGluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCys	22
QY	137	GACCAATCTCCCATGCTGCTCTCGACGCTTGCTTGAACAGGACCCAGACACCAAGGTT	196
DB	23	AspGlnValSerAspAlaValLeuAspAlaCysLeuAlaGlnAspProAspSerLysVal	42
QY	197	GCTCGCAAAATGCAACAGACAACTTGCTCATGCTTCGGAGAGATCACCAAG	256
DB	43	AlaCysGluThrCysThrLysThrAsnMetValMetValPheGlyGluIleThrThrLys	62
QY	257	GCCAAAGTTCACACAGAGATCGCTGCTGACACCTGACAGGACACCTCGTCTCA	316
DB	63	AlaThrValAspTyrGluLysIleValArgAspThrCysArgAspIleGlyPheIleSer	82
QY	317	AACGATGTGGGACTTGATGCTGACAACTGCAAGTCTCTTAAACATTGACGACGAGGC	376
DB	83	AspAspValGlyLeuaspAlaAspHisCysLysValLeuValAsnIleGluGlnInSer	102
QY	377	CCTGATATTGCCAGGGTGTGCGGCCACCTTTACCAAGAGACCCGAGGAATCGGTGCT	436
DB	103	ProAspIleAlaGlnGlyValHisGlyHisPheThrLysArgProGluValGlyAla	122
QY	437	GGAGACAGGTCACATGTTGCTATGCCACGAGCAAAACCCACAAATGATGCCATTG	496
DB	123	GlyAspGlnGlyIleMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeu	142
QY	497	AGTCATGTTCTTCAACTAACTCGGTGCTGCTCACCAGGTTCCGCAAGAACGCAACC	556
DB	143	ThrHisMetLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThr	162
QY	557	TGCCCATGTTGAGGCTGATGGGAAACCCAAAGTCACTGTTGAGTATTACATGACAC	616
DB	163	CysAlaTrpLeuArgProAspGlyLysThrGlnValThrIleGluTyrLeuAsnGluGly	182
QY	617	GGTGCCATGGTTCAGTTCGTGTCACACTGCTTATCTCCACCCCAACATGATGAGCT	676
DB	183	GlyAlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGluThr	202
QY	677	GTGACCAACGACGAAATTCAGCTGACCTCAAGGAGCATGTGATCAAGCGGTGATCCCG	736
DB	203	ValThrAsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIlePro	222
QY	737	GAGAAGTACCTTGATGAGAGACCAATTTCCACTTGAACCCCTCTCGCGCTTTGTGATT	796
DB	223	GlyLysTyrLeuAspGluAsnThrIlePheHisLeuAsnProSerGlyArgPheValIle	242
QY	797	GGAGTCTTCACGGTGATGCTGCTCACCAGCGCGCAAGATCATCATCTTACGGA	856
DB	243	GlyGlyProHisGlyAspAlaGlyLeuThrAlaArgLysIleIleIleAspThrThrGly	262
QY	857	GGATGGGTGCTCATGCTGCTGCTGCTTCTCCGGGAAGGATCCCAACCAAGTTCATAG	916
DB	263	GlyTrpGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArg	282
QY	917	AGTGTGCTTACATTTGACAGAGGCTGCTTAAGAGCATTTGCGCAAGTGGACTAGCAGA	976
DB	283	SerGlyAlaTyrIleAlaArgGlnAlaAlaLysSerIleIleAlaSerGlyLeuAlaArg	302
QY	977	AGTGTGATTTGCAAGTGTCTTATGCCATGTTGTCGCCGAGCTTTGTCTGTTGTT	1036

DB	303	ArgCysIleValGlnIleSerTyrAlaIleGlyValProGluProLeuSerValPheVal	322
QY	1037	GACACCTATGGCACCGGGAAGATCCATGATAAGGAGATTCTCAACATTGTGAAGGAGAAC	1096
DB	323	AspSerTyrGlyThrGlyLysIleProAspArgGluIleLeuLysLeuValLysGluAsn	342
QY	1097	TTTGATTTTCAGGCCCGGTATGATCTCCATCAACCTTGATCTCAAGAGGGGTGGGAATAAC	1156
DB	343	PheAspPheArgProGlyMetIleThrIleAsnLeuAspLeuLysGlyGly--Asn	361
QY	1157	AGTTTCTTCAAGACGCTGCTCATATGGACACTTTCGGCAGAGAGACCTGACTTCACATGG	1216
DB	362	ArgPheIleLysThrAlaAlaTyrGlyHisPheGlyArgAspAlaAspPheThrTrp	381
QY	1217	GAAGTGTCTCAAGCCCTCAAGTGGGAGAGAGGCC	1249
DB	382	GluValValLysProLeuLysPheAspLysAla	392
RESULT 10			
ID	AAW97744 standard; protein; 394 AA.		
XX			
AC	AAW97744;		
DT	21-MAY-1999 (first entry)		
XX			
DE	Wheat S-adenosylmethionine synthetase.		
XX			
KW	S-Adenosylmethionine synthetase; wheat; amino acid; lysine; threonine;		
KW	methionine; cysteine; isoleucine; transgenic plant; crop improvement;		
KW	food; feedstuff.		
OS	Triticum aestivum.		
XX			
PH	Key Location/Qualifiers		
FT	Misc-difference 93 /note= "encoded by AAR"		
FT	Misc-difference 150 /note= "encoded by CTY"		
FT	Misc-difference 155 /note= "encoded by ACS"		
FT	Misc-difference 282 /note= "encoded by CGY"		
FT	Misc-difference 290 /note= "encoded by CAR"		
XX			
PN	W09855601-A2.		
XX			
PD	10-DEC-1998.		
XX			
PF	05-JUN-1998; 98WO-US011692.		
XX			
PR	06-JUN-1997; 97US-0048771P.		
PR	12-JUN-1997; 97US-0049443P.		
XX			
PA	(DUPO ) DU PONT DE NEMOURS & CO E I.		
XX			
PI	Falco SC, Allen SM, Rafaleki JA, Hitz WD, Kinney AJ, Abell LM;		
PI	Thorpe CJ;		
XX			
DR	WPI; 1999-070263/06.		
DR	N-PSDB; AAX07185.		
XX			
PT	New plant amino acid biosynthetic enzymes, DNA and chimeric genes -		
PT	encode: dihydrodipicolinate reductase; diaminopimelate epimerase; threonine		
PT	synthase; threonine deaminase; S-adenosylmethionine synthetase.		
XX			
PS	Example 7; Page 70-71; 98pp; English.		
XX			
CC	This is the amino acid sequence of a full-length wheat S-		
CC	adenosylmethionine synthetase, as deduced from a cDNA contig (see		
CC	AAX07185) obtained from kernel, leaf, seedling and root cDNA clones. The		
CC	wheat enzyme shows sequence similarity to the barley enzyme. The		

invention relates to new isolated nucleic acid fragments (see AWO7468-85) encoding plant enzymes (see AWO7727-44) that catalyse steps in the biosynthesis of lysine, threonine, methionine, cysteine and isoleucine from aspartate, the enzyme being selected from dihydrodipicolinate reductase, diaminopimelate epimerase, threonine synthase, threonine deaminase or S-adenosylmethionine synthetase. The invention also relates to the construction of a chimeric gene encoding all or a portion of the biosynthetic pathway enzyme, in sense or antisense orientation, where expression of the chimeric gene results in production of altered levels of the enzyme in a transformed host cell. Overexpression or reduction of expression of genes encoding the amino acid biosynthetic pathway enzymes in crop plants such as corn, soybean and wheat can be used to alter levels of the amino acids in human food and animal feed. Transformed host cells can also be used to identify compounds that inhibit one of the enzymes

Sequence 394 AA;

Alignment Scores:		
Pred. No.:	1.45e-181	394
Score:	1891.50	355
Percent Similarity:	95.40%	Matches: 18
Best Local Similarity:	90.79%	Conservative: 17
Query Match:	68.83%	Indels: 1
DB:	2	Gaps: 1
US-10-734-698A-38 (1-1485)	x AAW97744 (1-394)	

US-10-734-698A-38 (1-1485) X AAW97744 (1-394)

77	Qy	GCAGAGACATTCCTATTACCTCAGAGTCAGTAACAGAGGGACACCTCTGACAAGACTCTGC	136
3	Db	AlaGluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCys	22
137	Qy	GACCAATCTCCGATCTCTCTCAGACGCTTGCTTGAACAGGACCCAGACAGCAAGGTT	196
23	Db	AspGlnValSerAspAlaValLeuAspAlaCysLeuAlaGlnAspAlaAspSerLysVal	42
197	Qy	GCTTCGGAACATGCAACCAAGACCAACTTGGTCATGGCTTTCGGAGAGATCACCAACAAG	256
43	Db	AlaCysGluThrValThrLysThrAsnMetValMetValLeuGlyGluIleThrThrLys	62
257	Qy	GCCAAAGTTCATACGAGAAGATCTGGTGACACCTCTCAGACACATCGGCTTCGCTCA	316
63	Db	AlaThrValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheIleSer	82
317	Qy	AACGATGTGGACTTGATGCTGCACAACTGCAAGGTCCTGTAAACATTGACGACGAGC	376
83	Db	AspAspValGlyLeuAspAlaAspArgCysLysValLeuValAsnIleGluGlnGlnSer	102
377	Qy	CCTGATATTGCCCGGGTGTGCACGGCCACTTACCAAAAGACCCGAGGAATCGGTGCT	436
103	Db	ProAspIleAlaGlnGlyValHisGlyHisPheThrLysArgProGluGluValGlyAla	122
437	Qy	GGAGACGAGGTCACATGTTTGGCTATGCGACGAGCAAAACCCAGAAATTGATGCCAATG	496
123	Db	GlyAspGlnGlyIleMetPheGlyTyralaThrAspGluThrProGluLeuMetProLeu	142
497	Qy	AGTCATGTTCTTGCAATAAATCCGGTGCTGCTCTCACCGAGGTTCCGAAGACCGAACC	556
143	Db	LysHisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValaArgLysAsnGlyThr	162
557	Qy	TGCCCATGTTGAGGCTCATCGGAAACCCCAAGTGACTGTTTGATGATTCAATGACAAC	616
163	Db	CysAlaTrpValArgProAspGlyLysThrGlnValThrValGluTyrLeuAsnGluAsp	182
617	Qy	GGTGCCATGGTTCAGTTCGTTCCACACTGTGCTTATCTCCACCCCAACATGATGAGCT	676
183	Db	GlyAlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGluThr	202
677	Qy	GTGACCAACGAGAAATTCACCTGACCTCAAGAGCATGTGATCAAGCCGGTGATCCCG	736
203	Db	ValThrAsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIlePro	222
737	Qy	GAGAAGTACCTTGATGAGAAGACCAATTTTCCACTTGAAACCCCTCTGGCCGCTTTGTCA	796

## Alignment Scores:

Pred. No.: 4,63e-181 Length: 394  
Score: 1886.50 Matches: 353  
Percent Similarity: 95.40% Conservative: 20  
Best Local Similarity: 90.28% Mismatches: 17  
Query Match: 68.65% Indels: 1  
DB: 2 Gaps: 1

US-10-734-698A-38 (1-1485) x AAW34541 (1-394)

```
QY 77 GCAGAGACATTCCTATTACCTCAGAGTCAAGTGAACGAGGACACCCCTGACAGCTCTGC 136
DB 3 AlaGluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCys 22

QY 137 GACCAATCTCCGATGCTGCTCTCGACGCTTGCCTTGAACAGGACCCAGACACCAAGGTT 196
DB 23 AspGlnValSerAspAlaValLeuAspAlaCysLeuAlaGlnAspAlaAspSerLysVal 42

QY 197 GCCTGGAAACATGCACCAAGACCAACTTGGTTCATCGTTCGAGAGATCACCAACAG 256
DB 43 AlaCysGluThrValThrLysThrAsnMetValMetValLeuGlyGluIleThrThrLys 62

QY 257 GCCAAGCTTGACTACGAGAGATCGCTGACACCTGCAGGAAACATCGCTTCTGCTCA 316
DB 63 AlaThrValAspLysThrLysLysIleValArgAspThrCysArgAsnIleGlyPheIleSer 82

QY 317 AACGATGTGGACTTGCATGCTGCAAACTGCAAGTCTCTTGAACATTCGAGCAGCAGC 376
DB 83 AspAspValGlyLeuAspAlaAspArgCysLysValLeuValAsnIleGluGlnIleSer 102

QY 377 CCTGATATTCGCCAGGTTGACGGCCACTTACCAAGACCCGAGGAATTCGGTGTCT 436
DB 103 ProAspIleAlaGlnGlyValHisGlyHisPheThrLysArgProGluGluValGlyAla 122

QY 437 GGAGACGAGGTCCATGTTGCTATGCCAGGACGAAACCCAGCAATTCGTCATG 496
DB 123 GlyAspGlnGlyIleMetPheGlyLysThrValThrAspGluThrProGluLeuMetProLeu 142

QY 497 AGTCATGTTCTTGCACAACTCCGCTGCTCTCACCAGGTTCCGCAAGAACGGAACC 556
DB 143 SerHisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThr 162

QY 557 TGCCCATGTTGAGGCTGATGGGAAACCCAAAGTGAATTCGTTGAGTATTCAATGACAAC 616
DB 163 CysAlaTrpValArgProAspGlyLysThrGlnValThrIleAsnThrLeuAsnGluAsp 182

QY 617 GGTGCCATGTTCCAGTTCGTGTCACATGCTGCTTATCTCCACCCCAACATGATGACT 676
DB 183 GlyAlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGluThr 202

QY 677 GTGACCAACGAGAAATTCAGCTGACCTCAAGGAGCATGTGATCAAGCCGGTGTATCCCG 736
DB 203 ValThrAsnAspGluLeuAlaAlaAspLeuLysGluHisValIleLysProValIlePro 222

QY 737 GAGAAGTACTTGATGAGAAGACCATTTTCCACTTGAACCCCTCTGCGCGTTTGTTCATT 796
DB 223 AlaLysThrLeuAspGluAsnThrIlePheHisLeuAsnProSerGlyArgPheValIle 242

QY 797 GGAGTCTCCAGGTCATGCTGCTCAGCGCCGCAAGATCATCATCATCTACGATACGGA 856
DB 243 GlyGlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrThrGly 262

QY 857 CGATGGGTGCTCATGGTGGTGGTCTTCTCGGGAAGGATCCCAACCAAGTTGATAGG 916
DB 263 GlyTrpGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArg 282

QY 917 AGTGGTCTTACATTTGAGACAGGCTGCTTAAGAGCAATTTGGCAAGTGCAGTACGACA 976
DB 283 SerGlyAlaThrIleAlaArgGlnAlaAlaLysSerIleIleAlaSerGlyLeuAlaArg 302

QY 977 AGTGCATTTGCAAGTGTCTTATGCCATTTGTTGCCCGAGCCTTTGCTGCTTTGTT 1036
DB 303 ArgCysIleValGlnIleSerThrAlaIleGlyValProGluProLeuSerValPheVal 322
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QY 1037 GACACCTATGGCACCGGGAAGATCCATGATAAAGGAGATTCTCAACATTTGTAAGGAGAAC 1096
DB 323 AspSerThrGlyThrGlyLysIleProAspArgGluIleLeuLysLeuValLysGluAsn 342

QY 1097 TTTGATTTTCAGGCCCGGATGATCTCCCATCAACCTTGATCTCAAGAGGGGTGGGAATAAC 1156
DB 343 PheAspPheArgProGlyMetIleThrIleAsnLeuAspLeuLysGlyGly---Asn 361

QY 1157 AGGTTCTTGAAGACTGCTCATATGACACTTTCGGCAGAGAGACCCCTGACTTTCACATGG 1216
DB 362 ArgPheIleLysThrAlaAlaThrGlyHisPheGlyArgAspAspAlaAspPheThrTrp 381

QY 1217 GAAGTGGTCAACCCCTCAAGTGGGAGAGAGGCC 1249
DB 382 GluValValLysProLeuLysPheAspLysAla 392

RESULT 12
AAG39107
ID AAG39107 standard; protein; 439 AA.
XX
AC AAG39107;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48341.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 28-APR-1999; 99US-0130891P.
PR 30-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 04-MAY-1999; 99US-0132407P.
PR 05-MAY-1999; 99US-0132484P.
PR 06-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 07-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135623P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
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Alignment Scores:
Pred. No.: 1,35e-179 Length: 390
Score: 1872.00 Matches: 348
Percent Similarity: 95.08% Conservative: 19
Best Local Similarity: 90.16% Mismatches: 19
Query Match: 68.12% Indels: 0
DB: 3 Gaps: 0

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QY 140 CAAATCTCCGATGCTCTCGACGCTTGCCTTGAACAGACCCAGACAGGAGTTGCC 199
DB 22 GinIleSerAspAlaIleLeuAspAlaCysLeuGluGlnAspProGluSerLysValAla 41
QY 200 TCGCAACATGACACCAAGACCACTTGGTCATGGTCTTCGGAGAGATCCACCAAGGCC 259
DB 42 CysGluThrCysThrLysThrAsnMetValMetValPheGlyGluIleThrThrAlaAla 61
QY 260 AAGCTTGACTACGAGAAAGTACGTCGTGACACCTGCGAGAAACATCGCTTCTCAAC 319
DB 62 LysValAspTyrGluLysIleValArgSerThrCysArgGluIleGlyPheIleSerAla 81
QY 320 GATGTGGGACTGATCTGACAACTGCAAGGTCCTTTGTAACATTTGAGCAGACGACCT 379
DB 82 AspValGlyLeuAspAlaAspLysCysAsnValLeuValAsnIleGluGlnSerPro 101
QY 380 GATATTGCCCGGCTGTCACGCGCACCTTACCAGAACCCGAGGAATCGGTCTGGA 439
DB 102 AspIleAlaGlnGlyValHisGlyHisLeuThrLysLysProGluAspIleGlyAlaGly 121
QY 440 GACCAAGGTCACATGTTTGGCTATGCCAGGAGAAACCCAGAAATTTGATGCTAGCT 499
DB 122 AspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuThr 141
QY 500 CATGTTCTTGCACAACTCGGTGCTGCTCTCACCGAGGTTGCGCAAGAACGGAACCTGC 559
DB 142 HisValLeuAlaThrLysLeuGlyAlaLysLeuThrGluValArgLysAsnLysThrCys 161
QY 560 CCATGTTGAGGCTGATCGGAACCCAGTCACTGTTGAGTATTACATCAACAGCT 619
DB 162 ProTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrLysAsnAspGlyGly 181
QY 620 GCATGTTCCGATTCGTTGTCACACTGTGCTTATCTCCACCAACATGATGAGACTG 679
DB 182 AlaMetIleProIleArgValHisThrValLeuIleSerThrGlnHisAspGluThrVal 201
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DB 202 ThrAsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIleProAla 221
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DB 222 LysTyrLeuAspAspAsnThrIlePheHisLeuAsnProSerGlyArgPheValIleGly 241
QY 800 GGTCTCAGGTCATGCTGCTCTCACCGCGCGCAAGATCATCATGATATTACGAGGA 859
DB 242 GlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleIleAspThrThrGlyGly 261
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DB 282 GlyAlaTyrIleValArgGlnAlaAlaLysSerValValAlaAlaGlyLeuAlaArg 301
QY 980 TGCATTGTGCAAGTGTCTTATGCCATTTGGTGTGCCGAGCCCTTGTCTCTTTGTGAC 1039
DB 302 CysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAsp 321
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DB 322 ThrTyrLysThrGlyThrIleProAspLysAspIleLeuValLeuIleLysGluAlaPhe 341
QY 1100 GATTTTCAGCCCGGTATGATCTCCATCAACCTTGTATCTCAAGAGGGTGGGAATAACAGG 1159
DB 342 AspPheArgProGlyMetMetAlaIleAsnLeuAspLeuLysArgGlyGlyAsnPheArg 361
QY 1160 TTCTTTGAAGACTGTGTCATATGGACATTCGCGCAGAGAGACCCCTGACTTTCATCGGAA 1219
DB 362 PheGlnLysThrAlaAlaTyrGlyHisPheGlyArgAspProAspPheThrTrpGlu 381
QY 1220 GTGGTCAAGCCCTCAAG 1237
DB 382 ValValLysProLeuLys 387

RESULT 14
AAY72078
ID AAY72078 standard; protein; 390 AA.
XX AAY72078;
XX 28-MAR-2001 (first entry)
XX Nicotiana tabacum S-adenosylmethionine synthetase (SAMS).
XX Tobacco; alkaloid; nicotine; transgenic plant; pharmaceutical protein;
XX herbicide resistance; S-adenosylmethionine synthetase; SAMS.
XX Nicotiana tabacum.
XX WO200067558-A1.
XX 16-NOV-2000.
XX 05-MAY-2000; 2000WO-US012450.
XX 06-MAY-1999; 99US-0132919P.
XX (TIMK/) TIMKO M.
XX Timko M;
XX WPI; 2001-007279/01.
XX N-PSDB; AAD02296.
XX New nucleic acid encoding alkaloid-synthesis enzymes in tobacco, useful
XX e.g. for producing transgenic plants with altered nicotine content.
XX Claim 17; Page 79-81; 103pp; English.
XX The invention relates to enzymes involved in alkaloid, specifically
XX nicotine, synthesis in tobacco and nucleic acids encoding them. The
XX nucleic acid of the invention can be used, in sense or antisense
XX orientation, to produce transgenic tobacco plants with altered alkaloid
XX content, and also for expression of exogenous proteins, e.g.
XX pharmaceutical proteins or proteins implicated in resistance to
XX herbicides. The protein of the invention can be used to identify
XX modulators of enzymatic activity in plants. The present sequence is
XX Nicotiana tabacum S-adenosylmethionine synthetase (SAMS). This enzyme is
XX involved in the nicotine biosynthetic pathway
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SQ Sequence 390 AA;				Db	302	CysileValGlnValSerTyrAlaileGlyValalaGluProLeuSerValPheValaAsp	321
Alignment Scores:				QY	1040	ACCTATGGCACCGGAGAGATCCATGATAAGAGAGATTCTCAACATTGTGAAGAGAACTTT	1099
Pred. No.:	2,71e-179	Length:	390	Db	322	ThrTyrIysThrGlyThrIleProAspIysAspileuThrLeuIleLysGluAsnPhe	341
Score:	1869.00	Matches:	348	QY	1100	GATTTACGGCCCGGTATGATCTCCATCAACCTTGATCTCAAGAGGGGTGGGAATAACAGG	1159
Percent Similarity:	94.82%	Conservative:	18	Db	342	AspPheArgProGlyMetMetSerIleAsnLeuAspLeuLeuArgGlyGlyAsnPheArg	361
Best Local Similarity:	90.16%	Mismatches:	20	QY	1160	TTCTTTGAAGACTGCTGCATATGGACACTTCGCGCAGAGAGGACCCCTGACTTCACATGGGAA	1219
Query Match:	68.01%	Indels:	0	Db	362	TyrGlnIysThrAlaIaIaTyrGlyHisPheGlyArgAspAspProAspPheSerTrpGlu	381
DB:	4	Gaps:	0	QY	1220	GTGGTCAAGCCCTCAAG	1237
US-10-734-698A-38 (1-1485) x AAY72078 (1-390)				Db	382	ThrValIysValLeuLys	387
QY	80	GAGACATTCCTATTACCTCAGAGTCAGTGAACGAGGACACCTGACAGAGCTCTCGCAC	139	RESULT 15			
Db	2	GluThrPheLeuPheThrSerGluSerValanGluGlyHisProAspIysLeuCysAsp	21	AAG40367			
QY	140	CAAAATCCGATCTGCTCTCGACGCTTCCTTGAACAGAGCCCGAGAGATCAACCAAGGTTGCC	199	ID	AAG40367	standard; protein; 344 AA.	
Db	22	GlnValSerAspAlaileLeuAspAlaCysLeuGluGlnAspProGluSerIysValaIa	41	XX	AAG40367;		
QY	200	TGCGAAACATGACCAAGACCAACTTGCTCATGCTTCGAGAGATCAACCAAGGCC	259	XX	18-OCT-2000	(first entry)	
Db	42	CysGluThrCysThrIysThrAsnMetValMetValPheGlyGluIleThrThrIysAla	61	DE	Arabidopsis	thaliana protein fragment SEQ ID NO: 50078.	
QY	260	AACGTTGACTACGAGAAGATCGTGGTGACACCTGCAGGAACATCGGCTTCGTCTCAAAC	319	KW	Protein identification; signal transduction pathway; metabolic pathway;		
Db	62	ThrValAspTyrGluLysIleValArgAspThrCysArgGlyIleGlyPheThrSerAla	81	KW	hybridisation assay; genetic mapping; gene expression control; promoter;		
QY	320	GATGTGGGACTTGATGCTGACAACTGCAAGTCTCTTTGTAACATTGAGCAGCAGCCCT	379	XX	termination sequence.		
Db	82	AspValGlyLeuAspAlaAspAsnCysIysValLeuValAsnIleGluGlnSerPro	101	OS	Arabidopsis	thaliana.	
QY	380	GATATTGCCAGGCTGACGGCCACCTTACAAAGACCCGAGAGAAATCGGCTCTGA	439	PN	EP1033405-A2.		
Db	102	AspileAlaGlnGlyValHisGlyHisLeuThrLysLysProGluGluIleGlyAlaGly	121	PD	06-SEP-2000.		
QY	440	GACGAGGTCACATGTTTCGGCTATGCCAGGACGAAACCCAGAAATTGATGCAATTGAT	499	PF	25-FEB-2000; 2000EP-00301439.		
Db	122	AspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuThr	141	PR	25-FEB-1999;	99US-0121825P.	
QY	500	CATGTTCTTTGCAACTGAACTCGGTGCTCTCTCACCGAGGTTTCGCAAGAACCGAACTGC	559	PR	05-MAR-1999;	99US-0123180P.	
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GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: August 25, 2005, 17:04:27 ; Search time 49 Seconds  
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Title: US-10-734-698A-38

Perfect score: 2748

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Searched: 513545 seqs, 74649064 residues

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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14	1061.5	38.6	396	3	US-09-273-686-2	Sequence 2, Appl
15	1055	38.4	395	4	US-09-328-352-6660	Sequence 6660, Ap
16	1042.5	37.9	415	3	US-09-134-001C-5077	Sequence 5077, Ap
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18	1028.5	37.4	402	2	US-08-403-852D-19	Sequence 19, Appl
19	1028.5	37.4	402	3	US-08-510-648B-20	Sequence 20, Appl
20	1028.5	37.4	402	3	US-09-231-818-19	Sequence 19, Appl
21	1028.5	37.4	402	4	US-09-635-359B-19	Sequence 2, Appl
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24	832	30.3	332	3	US-09-320-878-16	Sequence 20, Appl
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35	114	4.1	1140	4	US-09-538-092-647	Sequence 19032, A
36	113.5	4.1	328	4	US-09-252-991A-26345	Sequence 26207, A
37	112.5	4.1	481	4	US-09-252-991A-19032	Sequence 18676, A
38	110.5	4.0	781	4	US-09-252-991A-18676	Sequence 16667, A
39	108	3.9	271	4	US-09-252-991A-16667	Sequence 20377, A
40	107	3.9	492	4	US-09-902-540-16667	Sequence 26803, A
41	106	3.9	224	4	US-09-252-991A-20377	Sequence 26803, A
42	105.5	3.8	223	4	US-09-252-991A-26803	Sequence 18136, A
43	105.5	3.8	291	4	US-09-252-991A-18136	Sequence 21827, A
44	105	3.8	1093	4	US-09-252-991A-21827	Sequence 16771, A
45	104.5	3.8	393	4	US-09-252-991A-16771	

#### ALIGNMENTS

##### RESULT 1

US-09-424-978B-39  
; Sequence 39, Application US/09424978B  
; Patent No. 6664445  
; GENERAL INFORMATION:  
; APPLICANT: Falco, Saverio Carl  
; APPLICANT: Allen, Stephen M.  
; APPLICANT: Rafalski, J. Antoni  
; APPLICANT: Hitz, William D.  
; APPLICANT: Kinney, Anthony J.  
; APPLICANT: Abell, Lynne N.  
; TITLE OF INVENTION: Plant Amino Acid Biosynthetic Enzymes  
; FILE REFERENCE: BB-1087  
; CURRENT APPLICATION NUMBER: US/09/424,978B  
; CURRENT FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: US 60/048,771  
; PRIOR FILING DATE: 1997-06-06  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 39  
; LENGTH: 392  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-09-424-978B-39

Alignment Scores:  
Pred. No.: 7, 03e-211 Length: 392  
Score: 2083.00 Matches: 392  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 75.80% Indels: 0  
DB: 4 Gaps: 0

US-10-734-698A-38 (1-1485) x US-09-424-978B-39 (1-392)

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QY 74 ATGGCAGACATTCCTCTATTTTACCTCAGAGTCAGTGAACGAGGGACACCTGCACAGCTC 133
Db 1 MetAlaGluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeu 20
QY 134 TCGCACCAAATCTCCGATGCTGCTCTCGACGCTTGCCTTGAACAGGACCCAGACAGCAAG 193
Db 21 CysAspGlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLys 40
QY 194 GTTGCTGCGAAACATGACACCAAGACCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 253
Db 41 ValAlaCysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThr 60
QY 254 AAGGCCAACGTTGACTACGACAGAGATCGTGCCTGACACCTGACAGAAACATCGCTTCGTC 313
Db 61 LysAlaAsnValAspTyrGluLysIleValAlaGAspThrCysArgAsnIleGlyPheVal 80
QY 314 TCAACGATGTGGGACTTGATGCTGACAACTGCAAGCTCTTGTAAACATTTGAGCAGCAG 373
Db 81 SerAsnAspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGlnGln 100
QY 374 AGCCCTGATATTGCCCAGGGTGTGACGGCCACCTTACCAAAAGACCGAGGAATCGGT 433
Db 101 SerProAspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGly 120
QY 434 GCTGGAGACAGGTCACATGTTTGGCTATGTCACGAGCAAAACCCAGAAATTTGATGCCA 493
Db 121 AlaGlyAspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetPro 140
QY 494 TTGAGTCATGTTCTTGCAACTGAACTCGGTGCTGCTCACCAGGTTTGCAGGAACCGGA 553
Db 141 LeuSerHisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGly 160
QY 554 ACTGCCCCATGTTGAGCGCTGATGGGAAAACCCAAAGTCAGTGTGAGTATTACATGAC 613
Db 161 ThrCysProTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrThrAsnAsp 180
QY 614 AACGGTGCCATGTTCCAGTCTGCTGTCACACTGCTTATCTCCACCCCAACATGATGAG 673
Db 181 AsnGlyAlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGlu 200
QY 674 ACTGTGACCAACGACGAAATTTGAGCTGACCTCAAGGAGCATGTGATCAAGCGGTGATC 733
Db 201 ThrValThrAsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIle 220
QY 734 CGGAGAGTACTCTGATGAGAGACCATTTCCACTTGAACCCCTCGCCGCTTTGTC 793
Db 221 ProGluLysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheVal 240
QY 794 ATTGGAGTCTCACGGTCATGCTGCTCACCAGCGCAAGATCATCATGATCTTAC 853
Db 241 IleGlyGlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleIleAspThrTyr 260
QY 854 GGAGGATGGGTGCTCATGCTGCTGCTGCTTCTCCGGAAGGATCCCAACCAAGTTGAT 913
Db 261 GlyGlyTyrGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAsp 280
QY 914 AGAGTGGTCTTACATTTGTGACACAGGCTGCTTAAGAGCATTTGGCAAGTGCATGCC 973
Db 281 ArgSerGlyAlaTyrIleValArgGlnAlaAlaLysSerIleValAlaSerGlyLeuAla 300
QY 974 AGAAGTGCATTTGCAAGTGTCTTATGCTTGTGCTGCCGAGCTTTGCTGCTTT 1033
Db 301 ArgArgCysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPhe 320
QY 1034 GTTGACACCTATGGCACCGGAGATCCATGATAGAGGATTTCTCAACATTTGTGAAGGAG 1093
Db 321 ValAspThrTyrGlyThrGlyLysIleHisAspLysGluIleLeuAsnIleValLysGlu 340
QY 1094 ACTTTGATTTACGGCCCGGTATGATCTCCATCACTTGATCTCAAGAGGGGTGGGAT 1153
Db 341 AsnPheAspPheArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyGlyAsn 360
QY 1154 AACAGGTTCTTGAAGACTGCTGATATGACACTTTCGGCAGAGAGGACCTGACTTCA 1213
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Db 361 AsnArgPheLeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThr 380
QY 1214 TGGGAAGTGGTCAAGCCCTCAAGTGGGAGAGGCC 1249
Db 381 TrpGluValValLysProLeuLysTrpGluLysAla 392

RESULT 2
US-09-424-978B-36
; Sequence 36, Application US/09424978B
; Patent No. 6664445
; GENERAL INFORMATION:
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Allen, Stephen M.
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Hitz, William D.
; APPLICANT: Kinney, Anthony J.
; APPLICANT: Abell, Lynne N.
; APPLICANT: Thorpe, Catherine J.
; TITLE OF INVENTION: Plant Amino Acid Biosynthetic Enzymes
; FILE REFERENCE: BB-1087
; CURRENT APPLICATION NUMBER: US/09/424,978B
; CURRENT FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: US 60/046,771
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Zea mays
US-09-424-978B-36

Alignment Scores:
Pred. No.: 2,13e-196 Length: 396
Score: 1946.00 Matches: 363
Percent Similarity: 96.92% Conservative: 14
Best Local Similarity: 93.32% Mismatches: 12
Query Match: 70.82% Indels: 0
DB: 4 Gaps: 0

US-10-734-698A-38 (1-1485) x US-09-424-978B-36 (1-396)
QY 80 GAGACATTTCTATTACCTCAGAGTCAGTGAACGAGGGACACCTGCACAGCTCTGCAC 139
Db 5 AspThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCysAsp 24
QY 140 CAAATCTCCGATGCTGCTCCTCGACGCTTGCCTTGAACAGGACCCAGACAGCAAGTTC 199
Db 25 GlnValSerAspAlaValLeuAspAlaCysLeuAlaGluAspProAspSerLysValAla 44
QY 200 TCGGAAACATGCACAGACCAACATTTGCTCATGCTTTCGGAGAGATCACCACCAAGGCC 259
Db 45 CysGluThrCysThrLysThrAsnMetValMetValPheGlyGluIleThrThrLysAla 64
QY 260 AACCTTGACTACGAGAGATCGCTGACACCTGCAGAACATCGGCTTCGTCTCAAC 319
Db 65 AsnValAspTyrGluLysIleValArgGluThrCysArgAsnIleGlyPheValSerAsn 84
QY 320 GATGTGGACATTTGATGCTGACAACTGCAAGTCTCTTGAACATTTGAAACATTTGAGCAGAGCCCT 379
Db 85 AspValGlyLeuAspAlaAspHisCysLysValLeuValAsnIleGluGlnSerPro 104
QY 380 GATATTGCCAGGTGTGCACGGCCACCTTACCAAAAGACCCGAGGAAATCGGTGCTGGA 439
Db 105 AspIleAlaGlnGlyValHisGlyHisPheThrLysArgProGluGluIleGlyAlaGly 124
QY 440 GACCAGGTGCATGTTGGCTATGCCACGACGCAAAACCCAGAAATTCGTCATTGAGT 499
Db 125 AspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuSer 144
QY 500 CATGTTCTTGCAACTTAAACTCGGCTGCTCTCACCGAGGTTTCGCAAGACGGAACCTGCG 559
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Db 145 HisValLeuAlaThrLysLeuGlyAlaAArgLeuThrGluValAArgLysAenGlyThrCys 164  
Qy 560 CCATGGTTGAGCGCTGATGGGAAACCAAGTGAAGTCTGAGTATTACATGCAACAGGT 619  
Db 165 ProTrpLeuArgProAspGlyLysThrGlnValThrValGluThrArgAenGluGlyGly 184  
Qy 620 GCATGGTTCCAGTGTGTCACACGTGCTTATCTCCACCCCAACATGATGAGACTG 679  
Db 185 AlaMetValProIleArgValHisThrValLeuIleSerThrGlnHisAspGluThrVal 204  
Qy 680 ACCAAGCAGCAAAATGTCAGCTGACCTCAAGAGCATGTGATCAAGCGGTGATCCCGGAG 739  
Db 205 ThrAsnAspGluIleAlaAAspLeuLysGluHisValIleLysProIleIleProGlu 224  
Qy 740 AAGTACCTTCATGAGAGACCAATTTCCACTTGAACCCCTCTCGCGGTTTGTGATGGA 799  
Db 225 GlnTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheValIleGly 244  
Qy 800 GTCCTCACGGTGAATGTCATCCACGGCGCGCAAGATCATCATCATGATTCACGAGGA 859  
Db 245 GlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleIleAspThrTyrGlyGly 264  
Qy 860 TGGGGTGCATGCTGCTGCTCTCTCCGGAGGATCCACCAAGCTTGATAGAGT 919  
Db 265 TrpGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSer 284  
Qy 920 GTGCTTACATTTGTCAGACAGGCTGCTTAAGAGCATTTGTCAGAGTGGATAGCAGAAG 979  
Db 285 GlyAlaTyrValAlaAArgGlnAlaAlaLysSerIleValAlaSerGlyLeuAlaAArg 304  
Qy 980 TGCATTGTCAAGTGTCTTATGCCATTGGTGTGCCAGGCTTGTCTGTCTTTGTGAC 1039  
Db 305 AlaIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAsp 324  
Qy 1040 ACCTATGGCACCGGAGATCCATGATAGGAGATTTCAACATTTGAGAGGAGACTTT 1099  
Db 325 ThrTyrGlyThrGlyAlaIleProAspLysGluIleLeuLysIleValLysGluAenPhe 344  
Qy 1100 GATTTCAGGCGCGTATGATCTCCATCACTTGATCTCAAGAGGGTGGGAATACAGG 1159  
Db 345 AspPheArgProGlyMetIleIleIleAsnLeuAspLeuLysGlyAenGlyArg 364  
Qy 1160 TTCTGAAGACTCTGCATATGACACTTCGGCAGAGAGACCTTCATCATCGGAA 1219  
Db 365 TyrLeuLysThrAlaAlaTyrGlyHisPheGlyArgAspProAspPheThrTrpGlu 384  
Qy 1220 GTGCTCAAGCCCTCAAGTGGGAGAAG 1246  
Db 385 ValValLysProLeuLysSerGluLys 393

## RESULT 3

US-09-424-978B-42  
; Sequence 42, Application US/09424978B

; Patent No. 6664445

; GENERAL INFORMATION:

; APPLICANT: Falco, Saverio Carl

; APPLICANT: Allen, Stephen M.

; APPLICANT: Rafaleki, J. Antoni

; APPLICANT: Hitz, William D.

; APPLICANT: Kinney, Anthony J.

; APPLICANT: Abell, Lynne N.

; APPLICANT: Thorpe, Catherine J.

; TITLE OF INVENTION: Plant Amino Acid Biosynthetic Enzymes

; FILE REFERENCE: BB-1087

; CURRENT APPLICATION NUMBER: US/09/424,978B

; CURRENT FILING DATE: 1999-12-02

; PRIOR APPLICATION NUMBER: US 60/048,771

; PRIOR FILING DATE: 1997-06-06

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 42

; LENGTH: 394

; TYPE: PRT

; ORGANISM: Trifolium aestiva  
US-09-424-978B-42

## Alignment Scores:

Pred. No.: 1-226-190 Length: 394  
Score: 1891.50 Matches: 355  
Percent Similarity: 95.40% Conservatives: 18  
Best Local Similarity: 90.79% Mismatches: 17  
Query Match: 68.83% Indels: 1  
DB: 4 Gaps: 1

US-10-734-698A-38 (1-1485) x US-09-424-978B-42 (1-394)

Qy 77 GCAGAGACATTCCTATTATCTACCTCAGAGTCAGTGAACGAGGACACCTCACAAGCTCTGC 136  
Db 3 AlaGluThrPheLeuPheThrSerGluSerValAenGluGlyHisProAspLysLeuCys 22  
Qy 137 GACCAAACTCCGATGCTGCTCTCCACGCTTCCCTTGAACAGAGCCACAGCAGGTT 196  
Db 23 AspGlnValSerAspAlaValLeuAspAlaCysLeuAlaGlnAspAlaAspSerLysVal 42  
Qy 197 GCCTCGCAAAACATGCACCAAGACCAACTTGGTCTCATGCTCTCCGAGAGATCAACCAAG 256  
Db 43 AlaCysGluThrValThrLysThrAsnMetValMetValLeuGlyGluIleThrLys 62  
Qy 257 GCCAACGTTGATACGAGAGAATCGTGGCTGACACCTGCGAGAAACATCGGCTTCGCTCA 316  
Db 63 AlaThrValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheIleSer 82  
Qy 317 AACGATGGGACCTTGATGCTGACAACTGCAAGGTCCTTGTAAACATGAGCAGCAGAGC 376  
Db 83 AspAspValGlyLeuAspAlaAspArgCysLysValLeuValAsnIleGluGlnSer 102  
Qy 377 CCTGATATTCACGAGGCTGTCACGCGCCACCTTACCAAGACCCGAGAAATCGGTCT 436  
Db 103 ProAspIleAlaGlnGlyValHisGlyHisPheThrLysArgProGluGluValGlyAla 122  
Qy 437 GCAGACCAAGGTCACATGTTGGCTATGCCAGCGACGAAACCCCAAGAAATGATGCCATTG 496  
Db 123 GlyAspGlnGlyIleMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeu 142  
Qy 497 AGTCATGTTCTTGAACATAACTCGGTCGCTCTCACGAGGTCGCGAAGAACGAGAAC 556  
Db 143 LysHisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThr 162  
Qy 557 TGCCCATGTTGAGGCTGATGGGAAACCCCAAGGACTGTTGAGTATTACATGACAC 616  
Db 163 CysAlaTrpValArgProAspGlyLysThrGlnValThrValGluThrLeuAsnGluAsp 182  
Qy 617 GGTGCATGTTCCAGTTCGTCACACTGTGCTTATCTCCACCAACATGATGAGACT 676  
Db 183 GlyAlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGluThr 202  
Qy 677 GTGACCAACGAGAAATTCAGCTGACCTCAAGAGCATGTGATCAAGCGGTGATGCCG 736  
Db 203 ValThrAsnAspGluIleAlaAspLeuLysGluHisValIleLysProValIlePro 222  
Qy 737 GAGAAGTACCTTGATGAGAGACCACTTTCCACTTGAACCCCTCGCGGTTTCTCAT 796  
Db 223 AlaLysTyrLeuAspGluAsnThrIlePheHisLeuAenProSerGlyArgPheValIle 242  
Qy 797 GGAGGTCTCAGCGTGAATGCTGCTCACCGGCGCCCAAGATCATCATCATGATCTACGGA 856  
Db 243 GlyGlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleIleAspThrTyrGly 262  
Qy 857 GGATGGGTGCTCATGGTGGTGGTCTTCTCCGGGAAGGATCCCAAGGTTGATAGG 916  
Db 263 GlyTrpGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArg 282  
Qy 917 AGTGTGCTTACATTTGTGAGACAGCTGCTAAGACATTTGGGCAAGTGGACTAGCCAGA 976  
Db 283 SerGlyAlaTyrIleAlaArgGlnAlaAlaLysSerIleIleAlaSerGlyLeuAlaArg 302

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QY 977 AGGTGATGTCAGAGTGTCTTATGCTATGCTGTGTGCGCGACCTTTGTCTGTCTTGT 1036
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 303 ArgCysIleValGlnIleSerTyrAlaIleGlyValProGluProLeuSerValPheVal 322
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 1037 GACACTATGGACCGGGAAGATCCATGATTAAGGAGATCTCAACATTGTGAAGAGAAC 1096
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 323 AspSerTyrGlyThrGlyLysIleProAspArgGluIleLeuLysLeuValLysGluAen 342
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 1097 TTTGATTTCAGCGCCGGTATGCTCCATCACTTGCATCTCAAGAGGGTGGGAATAC 1156
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 343 PheAspPheArgProGlyMetIleSerIleAenLeuAspLeuLysGlyGly---Aen 361
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 1157 AGGTTCTTGAAGACTGCTCATATGACACTTCGGCAGAGAGACCCGTGACTTTCATG 1216
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 362 ArgPheIleLysThrAlaIleTyrGlyHisPheGlyArgAspAlaAspPheThrTrp 381
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 1217 GAAGTGGTCAAGCCCTCAAGTGGGAGAGGCC 1249
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 382 GluValValLysProLeuLysPheAspLysAla 392
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||

RESULT 4
US-09-949-016-10059
; Sequence 10059, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10059
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10059

Alignment Scores:
Pred. No.: 6,55e-130 Length: 416
Score: 1317.00 Matches: 260
Percent Similarity: 75.97% Conservative: 53
Best Local Similarity: 63.11% Mismatches: 87
Query Match: 47.93% Indels: 12
DB: Gaps: 5

US-10-734-698A-38 (1-1485) x US-09-949-016-10059 (1-416)
QY 8 CCCCACTCAACACACACCACTCTCTGCTCTTCTTCTACCTTCAAGTTTAAAGT 67
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 16 ProHisThrAspThrAsn-----MetAsnGlyGlnLeuAsnGlyPheHisGlu 31
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 68 ATTAAGATGGCAGAG---ACATTCTTATTTACTCAGAGTCAGTGAACGAGGACACCT 124
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 32 AlaPheIleGluGlyThrPheLeuPheThrSerGluSerValGlyGlyHisPro 51
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 125 GACAGCTCGGACCAATCTCGATGCTGCTCGAGCTTGCCTGGAACAGACCCCA 184
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 52 AspLysIleCysAspGlnIleSerAspAlaValLeuAspAlaHisLeuGlnGlnAspPro 71
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 185 GACAGCAGGTTCCTCGCAACATGACCAACATGACCAACCACTTGTGTCATGCTTCGAGAG 244
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 72 AspAlaLysValAlaCysGluThrValAlaLysThrGlyMetIleLeuLeuAlaGlyGlu 91
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 245 ATCAACCAAGCCCAACCTTGCTGACGAGAGAGATCGTGCCTGACACCTGCGAGAACATC 304
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
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Db 92 IleThrSerArgAlaAlaValAspTyrGlnLysValValArgGluAlaValLysHisIle 111
QY GCGTTCGTCTCAACGATGCGGACTTGATGCTGACAACTGCAAGTCTCTTGTAAACATT 364
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 112 GlyTyrAspAspSerLysGlyPheAspTyrLysThrCysAenValLeuValAlaLeu 131
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 365 GAGCAGCAGACCCCTGATATTATGCGCAGGCTGTGCACGGCCACCTTACCAGAAAGACCCCGAG 424
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 132 GluGlnGlnSerProAspIleAlaGlnGlyVal-----HisLeuAspArgAsnGluGlu 149
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 425 GAAATCGGTGCTGAGACCGAGGTCACATGTTTGGCTATGCCACGACGAAACCCAGAA 484
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 150 AspIleGlyAlaGlyAspGlnGlyLeuMetPheGlyTyrAlaThrAspGluThrGluGlu 169
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 485 TTGATGCCATTGAGTCATGTTCTTGCACAACTCGGTGCTGCTCTCACGAGGTTTCGC 544
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 170 CysMetProLeuThrIleValLeuAlaHisLysLeuAenAlaLysLeuAlaGluLeuArg 189
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 545 AAGAACGGAACTGCCCATGTTGAGGCTCATGGGAAACCCCAAGTGAAGTGTGAGTAT 604
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 190 ArgAsnGlyThrLeuProTrpLeuArgProAspSerLysThrGlnValThrValGlnTyr 209
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 605 TACAATGACAAACGGTGCCATGTTCCAGTTCGTGTCCACACTGTGCTTATCTCACCCAA 664
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 210 MetGlnAspArgGlyAlaValLeuProIleArgValHisThrIleValIleSerValGln 229
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 665 CATGATGAGACTGTGACCAACGACGAAATTCGACCTGACCTCAAGGACATGTGATCAAG 724
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 230 HisAspGluGluValCysLeuAspGluMetArgAspAlaLeuLysGluLysValIleLys 249
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 725 CCGGTGATCCCGGAGAGTACTTGTGAGAGAACCATTTTCCACTTGAAACCCCTCTGCG 784
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 250 AlaValValProAlaLysTyrLeuAspGluAspThrIleTyrHisLeuGlnProSerGly 269
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 785 CGTTTGTGTCATGAGGTCCTCACGGTGATGCTGGTCTCACCGCGCGCAAGATCATATC 844
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 270 ArgPheValIleGlyGlyProGlnGlyAspAlaGlyLeuThrGlyArgLysIleVal 289
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 845 GATCTTACGAGGATGGGTGCTCATGGTGGTGGTCTTCCGGGAGAGATCCCAACC 904
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 290 AspThrTyrGlyGlyTrpGlyAlaHisGlyGlyAlaPheSerGlyLysAspTyrThr 309
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 905 AAGTTGATGAGAGTGGTCTTACATTTGTGACAGAGGCTGCTAAGAGCATTTGTGCAAGT 964
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 310 LysValAspArgSerAlaAlaTyrAlaAlaArgTrpValAlaLysSerLeuValLysGly 329
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 965 GGACTAGCACGAGGTGCAATTTGTGCAAGTGTCTTATGCTTATGCTGTCGCCGAGCCTTTG 1024
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 330 GlyLeuCysArgValLeuValGlnValSerTyrAlaIleGlyValSerHisProLeu 349
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 1025 TCTGCTCTTTGACACCTATGCGACCGGGAAGATCCATGATAGGAGATTTCTCAACATT 1084
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 350 SerIleSerIlePheHisTyrGlyThrSerGlnLysSerGluArgGluLeuGluIle 369
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 1085 GTGAAGAGAACTTTGATTTCCAGGCCCGGTATGATCTCCATCAACCTTGTCTCAAGAGG 1144
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 370 ValLysLysAsnPheAspLeuArgProGlyValIleValArgAspLeuAspLeuLysLys 389
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 1145 GGTGGGAATAACAGGTTCTTGAAGACTGCTGCATATGACACTTCCGCGAGAGAGACCCCT 1204
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 390 -----ProIleTyrGlnArgThrAlaAlaTyrGlyHisPheGlyArgAsp----- 404
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 1205 GACTTCACATGGGAGGTGTCAGCCCTCAAGTGG 1240
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 405 SerPheProTrpGluValProLysLysLeuLysTyr 416
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
```

## RESULT 5

```
US-09-976-594-471
; Sequence 471, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
```

; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS

; FILE REFERENCE: PA-0041 US  
; CURRENT APPLICATION NUMBER: US/09/976,594  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: 60/240,409  
; PRIOR FILING DATE: 2000-10-12  
; NUMBER OF SEQ ID NOS: 1143  
; SOFTWARE: PERL Program  
; SEQ ID NO 471  
; LENGTH: 395  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Incyte ID No. 6673549 2600262CD1  
US-09-976-594-471

Alignment Scores:  
Pred. No.: 7,14e-130 Length: 395  
Score: 1316.50 Matches: 254  
Percent Similarity: 78.50% Conservative: 49  
Best Local Similarity: 65.80% Mismatches: 76  
Query Match: 47.91% Indels: 7  
DB: 4 Gaps: 3

US-10-734-698A-38 (1-1485) x US-09-976-594-471 (1-395)

QY 83 ACATTCTCTTTACCTCAGAGTCAGTGAACGAGGACACCCCTGACAGCTCTCGACCAA 142  
Db 17 ThrPheLeuPheThrSerGluSerValGlyGluGlyHisProAspLysIleCysAspGln 36  
QY 143 ATCTCCGATGCTCTCTCCGACGCTTGCCTTTGAACAGGACCCACAGCAAGGTTCCTGTC 202  
Db 37 IleSerAspAlaValLeuAspAlaHisLeuGlnGlnAspProAspAlaLysValAlaCys 56  
QY 203 GAAACATGACCAAGACCACTTGCTGTCATGCTTCCGAGAGATCAACCAAGGCCAAC 262  
Db 57 GluThrValAlaLysThrGlyMetIleLeuLeuAlaGlyGluIleThrSerArgAlaAla 76  
QY 263 GTTGACTACGAGAGATCGTCTGACACCTGACGAGCAATCGCTTCTCTCAACAGAT 322  
Db 77 ValAspTyrGlnLysValValArgGluAlaValLysHisIleGlyTyrAspSerSer 96  
QY 323 GTGGGACTTGATGCTGACAACTGCAAGTCTTGTAAACATTCAGCAGCAGACCTTGAT 382  
Db 97 LysGlyPheAspTyrLysThrCysAsnValLeuValAlaLeuGluGlnSerProAsp 116  
QY 383 ATGCCCAGGCTGTGACGGCCACCTTACCAAGACCCGAGAAATCGGTGCTGGAGAC 442  
Db 117 IleAlaGlnGlyVal-----HisLeuAspArgAsnGluAspIleGlyAlaGlyAsp 134  
QY 443 CAGGGTCACATGTTTGGCTATGCCAGGACGAAACCCAGAAATTTGATGCTTGTGAT 502  
Db 135 GlnGlyLeuMetPheGlyTyrAlaThrAspGluThrGluGluCysMetProLeuThrIle 154  
QY 503 GTTCTTGCAACTAACTCGGTGCTCGTCTCACCGAGGTTCGCAAGAACGGAACCTGCCCA 562  
Db 155 ValLeuAlaHisLysLeuAsnAlaLysLeuAlaGluLeuArgArgAsnGlyThrLeuPro 174  
QY 563 TGGTTGAGGCTGATGGGAAACCCAAAGTACCTGTTGAGTATTACATGACACCGTGGCC 622  
Db 175 TrpLeuArgProAspSerLysThrGlnValThrValGlnTyrMetGlnAspArgGlyAla 194  
QY 623 ATGGTTCGATGCTGTCACACTGTCTATCTCCACCAATCATGATGACTGTGACC 682  
Db 195 ValLeuProIleArgValHisThrIleValIleSerValGlnHisAspGluGluValCys 214  
QY 683 AACGCAAAATTCAGCTGACCTCAAGGAGCATGTGATCAAGCGGTGATCCCGGAGAAG 742  
Db 215 LeuAspGluMetArgAspAlaLeuLysGluLysValIleLysAlaValValProAlaLys 234  
QY 743 TACCTTGATGAGAAACCAATTTCCACTTGAAACCCCTCTGGCGGTTTGTCAATTGAGGT 802

Db 235 TyrLeuAspGluAspThrIleTyrHisLeuGlnProSerGlyArgPheValIleGlyGly 254  
QY 803 CCTCAGCGTGATGCTGCTCTCACCAGGCGCAAGATCATCATCATCATCATCATCATCAT 862  
Db 255 ProGlnGlyAspAlaGlyLeuThrGlyArgLysIleIleValAspThrTyrGlyGlyTrp 274  
QY 863 GGTGCTCATGCTGCTGCTTCTCCCGGGAAGATCCACCAGGTTTATAGGAGTGGT 922  
Db 275 GlyAlaHisGlyGlyAlaPheSerGlyLysAspTyrThrLysValAspArgSerAla 294  
QY 923 GCTTACATTTGTGACAGACGCTCTAAGACATTGTGGCAAGTGGACTAGCCAGAGTGC 982  
Db 295 AlaTyrAlaAlaArgTrpValAlaLysSerLeuValLysGlyGlyLysCysArgVal 314  
QY 983 ATTGTGCAAGTGTCTTATGCCATTGTGTGCCGAGCCTTTGTCTGTCTGTGTGACACC 1042  
Db 315 LeuValGlnValSerTyrAlaIleGlyValSerHisProLeuSerIleSerIlePheHis 334  
QY 1043 TATGGACCCGGAAGATCCATGATAGGAGATTCTCAACATTGTGTGAGGAGAACTTTGAT 1102  
Db 335 TyrGlyThrSerGlnLysSerGluArgGluLeuLeuGluIleValLysLysAsnPheAsp 354  
QY 1103 TTCAGGCCGCTGATGATCTCCATCAACCTTGATCTCAAGAGGGTGGGAATAACAGTTTC 1162  
Db 355 LeuArgProGlyValIleValArgAspLeuAspLeuLysLys-----ProIleTyr 371  
QY 1163 TTGAAGACTGTGCTATATGGACACTTCGGCAGAGAGACCCCTGACTTCACATGGGAAGTG 1222  
Db 372 GlnArgThrAlaAlaTyrGlyHisPheGlyArgAsp-----SerPheProTrpGluVal 389  
QY 1223 GTCAAGCCCTTCAAGTGG 1240  
Db 390 ProLysLysLeuLysTyr 395  
RESULT 6  
US-09-248-796A-18255  
; Sequence 18255, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS  
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 18255  
; LENGTH: 390  
; TYPE: PRT  
; ORGANISM: Candida albicans  
US-09-248-796A-18255  
Alignment Scores:  
Pred. No.: 4,51e-126 Length: 390  
Score: 1280.50 Matches: 242  
Percent Similarity: 77.00% Conservative: 56  
Best Local Similarity: 62.53% Mismatches: 82  
Query Match: 46.60% Indels: 7  
DB: 4 Gaps: 3  
US-10-734-698A-38 (1-1485) x US-09-248-796A-18255 (1-390)  
QY 80 GAGACATTTCTTATTTACCTCAGAGTCAGTGAACGAGGACACCCCTGACAGCTCTCGAC 139  
Db 11 GluThrPheLeuPheThrSerGluSerValGlyGluGlyHisProAspLysIleCysAsp 30  
QY 140 CAATCTCGATGCTGCTCTCGACCTTGTGACAGGACCCAGACAGGAGTGGC 199  
Db 31 GlnValSerAspAlaIleLeuAspAlaCysLeuAlaValAspProLeuSerLysValAla 50





Db 196 IleProValArgIleHisThrIleValIleSerValGlnHisAsnGluAspIleThrLeu 215  
QY 686 GACGAATTCAGCTGACCTCAAGGAGCATGTGATCAAGCCGGTGTATCCCGGAGAGTAC 745  
Db 216 GluGluMetArgAlaLeuLysGluGlnValIleArgAlaValProAlaLysTyr 235  
QY 746 CTTGATGAGAGACCAATTTCCATTGAACCCCTCTGGCGGTTTGTCTCATTTGAGGTCTT 805  
Db 236 LeuAspGluAspThrValTyrHisLeuGlnProSerGlyArgPheValIleGlyGlyPro 255  
QY 806 CACGGTGATGCTGCTCACCAGCCGCAAGATCATCATGATATTCAGGAGTGGGCT 865  
Db 256 GlnGlyAspAlaGlyValThrGlyArgLysIleValIleValAspThrTyrGlyGlyTrpGly 275  
QY 866 GCTCATGGTGGTGGTCTTTCTCCGGGAAGGATCCCAAGGTTGATAGGAGTGGTCT 925  
Db 276 AlaHisGlyGlyAlaPheSerGlyLysAspTyrThrLysValAspArgSerAlaAla 295  
QY 926 TACATTGTGAGACAGGCTGCTAAGACATTGTGGCAAGTGGACTACCGAAGGTCATT 985  
Db 296 TyrAlaAlaArgTrpValAlaLysSerLeuValLysAlaGlyLeuCysArgValLeu 315  
QY 986 GTGCAAGTGTCTATGCCATGCTGTGCGCGAGCTTTGTCTCTCTTTGTGACACCTAT 1045  
Db 316 ValGlnValSerTyrAlaIleGlyValAlaGluProLeuSerIleSerIlePheThrTyr 335  
QY 1046 GGCACCGGAAGATCCATAGGAGATTCTCAACATTGTGAAGAGAACTTTGATTTC 1105  
Db 336 GlyThrSerGlnLysThrGluArgGluLeuLeuAspValValHisLysAsnPheAspLeu 355  
QY 1106 AGCCCGGTATGATCTCCATCAACCTTGATCTCAAGAGGGGTGGGAATAACAGGTTCTTG 1165  
Db 356 ArgProGlyValIleValArgAspLeuAspLeuLysLys-----ProIleTyrGln 372  
QY 1166 AGACTGCTGCATATCGACACTTCGCGAGAGGAGCCCTGACTTCATCGGAGAGTGGTC 1225  
Db 373 LysThrAlaCysTyrGlyHisPheGlyArgSer-----GluPheProTrpGluValPro 390  
QY 1226 AAGCCCTC 1234  
Db 391 ArgLysLeu 393  
RESULT 8  
US-09-949-016-7658  
; Sequence 7658, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7658  
; LENGTH: 401  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-7658  
Alignment Scores:  
Pred. No.: 1,98e-125 Length: 401  
Score: 1274.50 Matches: 241  
Percent Similarity: 78.85% Conservative: 61  
Best Local Similarity: 62.92% Mismatches: 74  
Query Match: 46.38% Indels: 7

DB: 4 Gaps: 3  
US-10-734-698A-38 (1-1485) x US-09-949-016-7658 (1-401)  
QY 86 TTCCTATTACCTCAGAGTCACTGAACGAGGAGCACCCTGACAAGCTCTCGGACCAATC 145  
Db 24 PheMetPheThrSerGluSerValGlyGluGlyHisProAspLysIleCysAspGlnIle 43  
QY 146 TCCGATGCTGCTCCTCGACGCTTGAACAGAGGCCACAGACGAGCAAGGTGCTCGCGAA 205  
Db 44 SerAspAlaValLeuAspAlaHisLysGlnAspProAsnAlaLysValaLysGlu 63  
QY 206 ACATGCACCAAGACCACTGTGCTCATGTCTTCGAGAGATCACCAAGGCCAACGTT 265  
Db 64 ThrValCysLysThrGlyMetValLeuLeuCysGlyGluIleThrSerMetAlaMetVal 83  
QY 266 GACTACGAGAAATCGTGGTGCACACCTGCAGGAACATCGGCTTCGCTCAACAGATGTG 325  
Db 84 AspTyrGlnArgValValArgAspThrIleLysHisIleGlyTyrAspSerAlaLys 103  
QY 326 GGACTTGTGCTGACAACTGCAAGGTCTTGTAAACATTGAGCAGCAGACCCCTGATATT 385  
Db 104 GlyPheAspPheLysThrCysAsnValLeuValAlaLeuGluGlnSerProAspIle 123  
QY 386 GCCCAGGGTGTGCACGCGCACCTTACCAAAAGACCCGAGGAATCGGTCTCGAGACCAAG 445  
Db 124 AlaGlnCysVal-----HisLeuAspArgAsnGluGluAspValGlyAlaGlyAspGln 141  
QY 446 GGTACATGTTTGGTATGCCACGACGACCAACCCAGAAATTCATGCCATTGAGTCATGT 505  
Db 142 GlyLeuMetPheGlyTyrAlaThrAspGluThrGluGluCysMetProLeuThrIleIle 161  
QY 506 CTTGCAACTAACTCGGTCTGCTCACCGAGGTTCGCAAGACCGAACCTGCCCATCGG 565  
Db 162 LeuAlaHisLysLeuAsnAlaArgMetAlaAspLeuArgSerGlyLeuLeuProTrp 181  
QY 566 TTGAGGCTGATGGGAAACCAAGTACTGTGTAGTATTACAATGACAAACCGTGCATG 625  
Db 182 LeuArgProAspSerLysThrGlnValThrValGlnTyrMetGlnAspAsnGlyAlaVal 201  
QY 626 GTTCCAGTTCGTGTCACACTGTGCTTATCTCCACCCACATGATGAGACTGTGACCAAC 685  
Db 202 IleProValArgIleHisThrIleValIleSerValGlnHisAsnGluAspIleThrLeu 221  
QY 686 GACGAATTCAGCTGACCTCAAGGAGCATGTGATCAAGCCGGTGTATCCCGGAGAGTAC 745  
Db 222 GluGluMetArgArgAlaLeuLysGluGlnValIleArgAlaValProAlaLysTyr 241  
QY 746 CTTGATGAGAAGACCAATTTCCATTGAACCCCTCTGGCGGTTTGTCTCATTTGAGGTCT 805  
Db 242 LeuAspGluAspThrValTyrHisLeuGlnProSerGlyArgPheValIleGlyGlyPro 261  
QY 806 CACGGTGTGCTGCTCACCAGCCGCAAGATCATCATGATTCATCGGAGGATGGGT 865  
Db 262 GlnGlyAspAlaGlyValThrGlyArgLysIleValIleValAspThrTyrGlyGlyTrpGly 281  
QY 866 GCTCATGTTGTTGCTTCTCCGGGAAGGATCCCAAGTGTGATAGGAGTGGTCT 925  
Db 282 AlaHisGlyGlyAlaPheSerGlyLysAspTyrThrLysValAspArgSerAlaAla 301  
QY 926 TACATTGTGACAGGCTGCTAAGAGCATTTGTGGCAAGTGGAGTACGACCAAGAGTGCATT 985  
Db 302 TyrAlaAlaArgTrpValAlaLysSerLeuValLysAlaGlyLeuCysArgValLeu 321  
QY 986 GTGCAAGTGTCTTATGCCATTTGGTGTGCGCGAGCTTTGTCTCTTTGTGACACCTAT 1045  
Db 322 ValGlnValSerTyrAlaIleGlyValAlaGluProLeuSerIleSerIlePheThrTyr 341  
QY 1046 GGCACCGGAAGATCCATGATAAGGAGATTCTCAACATTGTGAAGAGAACTTTGATTTC 1105  
Db 342 GlyThrSerGlnLysThrGluArgGluLeuLeuAspValValHisLysAsnPheAspLeu 361  
QY 1106 AGGCCGCTATGATCTCCATCAACCTTGTATCTCAAGAGGGGTGGGAATAACAGGTTCTTG 1165



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Db      362 ArgProGlyValIleValArgAspLeuAspLeuLysLys-----ProlletyrGln 378
QY      1166 AAGACTCTGCATATGGACACTTCGGCGAGAGAGACCCTGACTTTCATCATGGGAAGTGTC 1225
Db      379 LysThrAlaCysTyrrGlyHisPheGlyArgSer-----GlutPheProtTrpGluValPro 396
QY      1226 AAGCCCTC 1234
Db      397 ArgLysLeu 399

RESULT 9
US-09-107-532A-6821
; Sequence 6821, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;                 ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6821:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 404 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...404
; SEQUENCE DESCRIPTION: SEQ ID NO: 6821:
US-09-107-532A-6821

Alignment Scores:
Pred. No.:          2.65e-107           Length:         404
Score:             1103.00              Matches:        224
Percent Similarity: 72.45%               Conservative:    60
Best Local Similarity: 57.14%            Mismatches:     94
Query Match:       40.14%                Indels:         14
DB:                  4                    Gaps:           5

US-10-734-698A-38 (1-1485) x US-09-107-532A-6821 (1-404)
QY      68 ATTAAGATGCCAGAGACATTCTTATTTCCTGACGTGACGTGAACGGAGCACCCCTGC 127

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181 Db -----IleValGlyIleAspAlaValValLeuSerThrGlnHisAlaGluAspIleSer 198
683 QY AACGACGAATTCGCAGCTGCATCAAGCGCATGTGATCAAGCCGGTGCATCCCGGAGAAG 742
199 Db GlnlysAspLeuHisGluAlaValMetGluLufellellyPheProIleuLeuProThrGlu 218
743 QY TACTTTGATGAGAAACACATTTCCTCCTTGAAACCCTCTGSCCGTTTTGTCTATTGGAGGT 802
219 Db TrpLeuAsnGluGlnThrLysTyrrPheIleAsnProThrGlyArgPheValIleGly 238
803 QY CCTCACGGTGATGCTGCTCACC CGGCCCGCAAGATCATCATCGATACTTACGGAGGATGG 862
239 Db ProMetGlyAspCysGlyLeuThrGlyArgLysIleIleValAspThrThrTyrrGlyMet 258
863 QY GTTGCTCATGCTGCTGCTGCTTCTCCGGGAAGGATCCCACCAAGTTGATAGGAGTGGT 922
259 Db AlaArgHisGlyGlyAlaPheSerGlyLysAspProSerLysValAspArgSerAla 278
923 QY GCTTACATTGTGAGACAGGCTGCTTAAGAGCATTTGTGCAAGTGGACGACCCAGAGAGTGC 982
279 Db AlaTyrrAlaAlaArgTyrrValAlaLysAsnIleValAlaAlaGlyLeuAlaAspArgCys 298
983 QY ATTGTCAAAGTGTCTTATGTCATTTGTGTGCCCCAGCGTTTGTCTGCTCTTTGTTGCACACC 1044
299 Db GluIleGlnValSertyrAlaIleGlyValAlaGluProThrSerIleMetValGluThr 318
1043 QY TATGGCACCGGGAAGATCCATGATTAAGGAGATTCTCAACATTTGTGAAGGAGAACCTTCAT 1104
319 Db PheGlyThrGluLysIleProThrSerGlnLeuIleLeuValArgGluPhePheAsp 338
1103 QY TTCAGGCC---GGTATGATCTCCATCAACCTTGATCTCAAGGGGTGGGAATAACAAGG 1155
339 Db LeuArgProTyrrGlyLeuIleGlnMet---LeuAspLeuLeu-----HisProIle 354
1160 QY TTCTTGAAGACTGCTGCATATGACACTTCGGCAGAGAGGACCTGACTTCACATGGGAA 1219
355 Db TyrGlnLysThrAlaAlaTyrrGlyHisPheGlyArg-----AlaGluPheProTrpGlu 372

RESULT 11
US-09-489-039A-11917
; Sequence 11917, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBS
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11917
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11917

Alignment Scores:
Pred. No.: 1,13e-103 Length: 385
Score: 1068.50 Matches: 223
Percent Similarity: 71.39% Conservative: 54
Best Local Similarity: 57.47% Mismatches: 92
Query Match: 38.88% Indels: 19
DB: Gaps: 8

US-10-734-698A-38 (1-1485) x US-09-489-039A-11917 (1-385)
QY 89 CTAATTTACCTCAGACTCAGTGAACGAGGACACCTGACAGAGCTCTCGGACCAATCTCC 148
Db 6 LeuPheThrSerGluSerValSerGluGlyHisProAspLysIleAlaAspGlnIleSer 25

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QY 188 AGCAGGTTGCTCCGGAACATGACCAAGACCAACTTGTGTCTCATGGTCTTCGAGAGATC 247
Db 48 AlahisValaalaGluThrAlaValThrGlySerValHisValPheGlyGluIle 67
QY 248 ACCACCAAGCCCAAGTTGACTACGAGAAGATCGTGCACACCTGCAGGACATCCGCC 307
Db 68 SerThrAsnAlaTyrValAspIleAsnArgValValArgAspThrIleAlaGluIleGly 87
QY 308 TTCGTCTCAACAGATGGGACTTGATGCTGCACCACTGCAAGGTCTTGTAAACATTGAG 367
Db 88 TyrThrAsnThrGluTyrGlyPheSerAlaGluThrValGlyValHisProSerLeuVal 107
QY 368 CAGCAGAGCCCTGATATGCTCCAGGGTGTGCAC-----GGCCACCTT 409
Db 108 GluGlnSerProAspIleAlaGlnGlyValAsnGluAlaLeuGluValArgGlyAsnAla 127
QY 410 ACCAAAGACCC--GAGGAAATCGGTCTGGAGACAGGAGTCCACATGTTTGTCTATGCC 466
Db 128 AspGlnAspProLeuAspLeuIleGlyAlaGlyAspGlnGlyLeuMetPheGlyPheAla 147
QY 467 ACGGACGAAACCCAGAAATTGATGCCATTCAGTTCATGTTCTTGCACCTAACTTCGGTGT 526
Db 148 ValAspGluThrGluGluLeuMetProLeuProIleAlaLeuSerHisLysLeuValArg 167
QY 527 CGTCTACCCAGGTTGCAAGAACCGAACCCTGCCCATGTTGAGGCTGTATGCGGAAAC 586
Db 168 ArgLeuAlaGluLeuArgLysSerGlyGluIleSerTyrLeuArgProAspAlaLysSer 187
QY 587 CAAGTCACTGTTGAGTAT---TACAATGACAAAGTGCCTGTTCCAGTTCGTGTCAC 643
Db 188 GlnValThrValGluTyrAspGluAsnAspArg-----ProValArgValAsp 203
QY 644 ACTGTGCTTATCTCCACCAACATGATGACTGTGCACCAACGCAAAATTCAGCTGAC 703
Db 204 ThrValValIleSerThrGlnHisAspProGluAlaThrAsnGluGlnIleHisGlnAsp 223
QY 704 CTCAGGAGCATGTGATCAAGCCGGTGATCCCGGAAAGTACTTGTATGAGAAGACCAT 763
Db 224 ValIleAspLysValIleLysGluValIleProSerSerTyrLeuAspAspLysThrLys 243
QY 764 TTCACCTTGAAACCTCTGCGCCCTTTGTCATTTGGAGGTCTTCACGGTGTATGCTGCTC 823
Db 244 PhePheIleAsnProThrGlyArgPheValIleGlyProGlnGlyAspSerGlyLeu 263
QY 824 ACCGGCGGCAAGATCATCATGACTTACGAGGATGGGGTCTCATGCTGTGTGTGCT 883
Db 264 ThrGlyArgLysIleIleValAspThrTyrGlyTyrSerArgHisGlyGlyAla 283
QY 884 TTCCTCGGGAAGATCCCAAGTTGATAGAGTGGTGTTCATTTGAGACAGGCT 943
Db 284 PheSerGlyLysAspAlaThrLysValAspArgSerAlaSerTyrAlaAlaArgTyrIle 303
QY 944 GCTAAGGCAATTTGCAAGTGCATGACAGGATGATGATGATGATGATGATGATGATGAT 1003
Db 304 AlaLysAsnIleValAlaGlyLeuAlaLysLysAlaGluValGlnLeuAlaTyrAla 323
QY 1004 ATTGGTGTGCGGAGCTTGTCTGTTGTTGACCTATGACCGCGGAGAGATCCAT 1063
Db 324 IleGlyValAlaGlnProValSerValArgIleAspThrPheGlyThrGlyThrValAla 343
QY 1064 GATAAGGAGATTCACATTTGTAAGGAGAACTTTGATTTTCAAGCCCGGTATGATCTCC 1123
Db 344 GluSerGlnLeuLysAlaAlaArgGlnIlePheAspLeuArgProAlaGlyIleIle 363
QY 1124 ATCAACTTGATCTCAAGAGGGTGGGAATAACAGGTTTCTTGNAGACTCTGCTGATATGA 1183
Db 364 GlnMetLeuAspLeuLysArg-----ProIleTyrArgGlnThrSerAlaTyrGly 380
QY 1184 CACTTCGGCAGAGACCTGACTTCACATGGGAA 1219
Db 381 HisMetGlyArgThrAspIleAspLeuProTrpGlu 392
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RESULT 13

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US-09-583-110-2778
; Sequence 2778, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 2778
; LENGTH: 396
; TYPE: PRN
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-2778
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Alignment Scores:  
Pred. No.: 4,98e-103 Length: 396  
Score: 1062.50 Matches: 218  
Percent Similarity: 70.77% Conservative: 58  
Best Local Similarity: 55.90% Mismatches: 99  
Query Match: 38.68% Indels: 15  
DB: 4 Gaps: 5

US-10-734-698a-38 (1-1485) x US-09-583-110-2778 (1-396)

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QY 134 TCGCACCAAAATCTCCGATGCTCTCTCCAGCGTTCCTTGAACAGGACCCAGCACAAG 193
Db 21 AlaAspGlnIleSerAspAlaIleLeuAspAlaIleLeuAlaLysAspProGluAlaHis 40
QY 194 GTTGCTCGGAAACATGACCAAGACCAACTTGGTGTGTCATGCTTCGAGAGATCCACC 253
Db 41 ValAlaAlaGluThrAlaValTyrThrGlySerValHisValPheGlyGluIleSerThr 60
QY 254 AAGGCCAACGTTGACTACGAGAAGATCGTGGTGACACCTGCAGGAAACATCGGCTTC 313
Db 61 AsnAlaTyrValAspIleAsnArgValValArgAspThrIleAlaGluIleGlyTyrThr 80
QY 314 TCAACACGATGCGGACTTGTATGCTGCACCAACTGCACAGGTCTTGTAAACATTCAGCAGCAG 373
Db 81 AsnThrGluTyrGlyPheSerAlaGluThrValGlyValHisProSerLeuValGluGln 100
QY 374 AGCCCTGATATTTGCCAGGGTGTGCAC-----GGCCACCTTACCACA 415
Db 101 SerProAspIleAlaGlnGlyValAsnGluAlaLeuGluValArgGlyAsnAlaAspGln 120
QY 416 AGACCC---GAGGAATCGTCTCGAGACCAAGGTCACATGTTTGGCTATCCACGAC 472
Db 121 AspProLeuAspLeuIleGlyAlaGlyAspGlnGlyLeuMetPheGlyPheAlaValAsp 140
QY 473 GAAACCCACAGATTCATGCTCATTTGATCATGTTTGCACCTTAAACCTCGTCTGCTCTC 532
Db 141 GluThrGluGluLeuMetProLeuProIleAlaLeuSerHisLysLeuValArgArgLeu 160
QY 533 ACCGAGGTTCCGAGAACCGAACCTGCCCATGTTGAGCCTGTATGGGAAACCAAGTG 592
Db 161 AlaGluLeuArgLysSerGlyGluIleSerTyrLeuArgProAspAlaLysSerGlnVal 180
QY 593 ACTGTTGAGTAT---TACAATGACAAACGTCGCATGTTCCAGTTCGTTCCACACTGTG 649
Db 181 ThrValGluTyrAspGluAsnAspArg-----ProValArgValAspThrVal 196
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QY 650 CTTATCTCCACCAACATGATGAGACTGTGACCAACGAGCAAGTTCAGCTGACCTCAAG 709
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
197 ValIleSerThrGlnHisAspProGluAlaThrAsnGluGlnIleHisGlnAspValIle 216
QY 710 GAGCATGTGATCAAGCCGCTGATCCGGAGAAAGTACCTTGTATGAGAAGACCATTTTCCAC 769
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
217 AspLysValIleLysGluValIleProSerSerTyrLeuAspAspLysThrLysPhe 236
QY 770 TTGAACCCCTCTGGCGGTTTCTCATTTGGAGTCTCTCAGGTGATGCTGCTTCCACCGGC 829
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
237 IleAsnProThrGlyArgPheValIleGlyGlyProGlnGlyAspSerGlyLeuThrGly 256
QY 830 CCAGATCATCATCATGATCTTACGAGGATGGGTGCTCATGGTGGTGGTCTTCTCC 889
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
257 ArgLysIleValAspThrTyrGlyGlyTyrSerArgHisGlyGlyGlyAlaPheSer 276
QY 890 GCGAAGGATCCCAACCAAGTTCATAGGAGTGTGCTTACATTTGTGAGCAGGCTCTCAAG 949
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
277 GlyLysAspAlaThrLysValAspArgSerAlaSerTyrAlaAlaArgTyrIleAlaLys 296
QY 950 AGCATTTGGCAAGTGGACTACCCAGAGAGTGCATTTGTGCAAGTGTCTTATGCCATTGGT 1009
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
297 AsnIleValAlaAlaGlyLeuAlaLysLysAlaGluValGlnLeuAlaTyrAlaIleGly 316
QY 1010 GTGCCCGAGCCTTGTCTCTTGTGACACTATGGCACCAGGAGATCCATCATGAAG 1069
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
317 ValAlaGlnProValSerValArgIleAspThrPheGlyThrGlyThrValAlaGluSer 336
QY 1070 GAGATTCTCAACATTTGCAAGGAGAACTTTGATTTTCAGGCCCGGTATGATCTCCATCAAC 1129
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
337 GlnLeuGluLysAlaAlaArgGlnIlePheAspLeuArgProAlaGlyIleIleGlnMet 356
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Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
357 LeuAspLeuLysArg-----ProIleTyrArgGlnThrSerAlaTyrGlyHisMet 373
QY 1190 GCGCAGAGAGCCCTGACTTCACATGGGAA 1219
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374 GlyArgThrAspIleAspLeuProThrGlu 383
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## RESULT 14

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US-09-273-686-2
; Sequence 2, Application US/09273686
; Patent No. 6228625
; GENERAL INFORMATION:
; APPLICANT: Zalacain, Magdalena
; APPLICANT: Burnham, Martin K. R.
; APPLICANT: Biswas, Sanjoy
; APPLICANT: Brown, James
; APPLICANT: Ingraham, Karen, A.
; APPLICANT: Chalker, Allison F.
; APPLICANT: So, Chi Y.
; APPLICANT: Holmes, David J.
; APPLICANT: Van Horn, Stephanie
; APPLICANT: Warren, Richard L.
; TITLE OF INVENTION: meck
; FILE REFERENCE: GM01076
; CURRENT APPLICATION NUMBER: US/09/273,686
; CURRENT FILING DATE: 1999-03-22
; EARLIER APPLICATION NUMBER: 60/106,767
; EARLIER FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-273-686-2
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Alignment Scores:
Pred. No.: 6,35e-103 Length: 396
Score: 1061.50 Matches: 218
Percent Similarity: 70.77% Conservative: 58
```

```
Best Local Similarity: 55.90% Mismatches: 99
Query Match: 38.63% Indels: 15
Db: 3 Gaps: 5

US-10-734-698A-38 (1-1485) x US-09-273-686-2 (1-396)

QY 74 ATGCAGAGACATTCCTTATTTACCTCAGAGTCAGTGAACGAGGACACCCCTGACAAAGCTC 133
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 MetSerGluArgLysLeuPheThrSerGluSerValSerGluGlyHisProAspLysIle 20
QY 134 TGCAGCAAAATCTCCGATGCTCTCCTCGACCTTGCCTTGAACAGGACCCAGACAGCAAG 193
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
21 AlaAspGlnIleSerAspAlaIleLeuAspAlaIleLeuAlaLysAspProGluAlaHis 40
QY 194 GTTCCTCGCAAAATGCACCAAGACCACTTGTGTCATGCTTCGCGAGAGATCACACC 253
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
41 ValAlaAlaGluThrAlaValTyrThrGlySerValHisValPheGlyGluIleSerThr 60
QY 254 AAGCCCAACGTTGACTACGAGAAGATCGTGGTGCACACCTCGCAGCAACATCGGCTTCGTC 313
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 AsnAlaTyrValAspIleAsnArgValValArgAspThrIleAlaGluIleGlyTyrThr 80
QY 314 TCAAACGATGTGGAGCTTGTATGCTGCACAACTGCAAGGTCTTGTAAACATTCAGCAGCAG 373
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
81 AsnThrGluTyrGlyPheSerAlaGluThrValGlyValHisProSerLeuValGluGln 100
QY 374 AGCCTGTATATGGCCAGCGGTGTGCAC-----GGCCACCTTACCAAA 415
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
101 SerProAspIleAlaGlnGlyValAsnGluAlaLeuGluValArgGlyAsnAlaAspGln 120
QY 416 AGACCC---GAGGAAATCGGTGCGAGACAGCGGTCACTGTTTGGCTATGCCACCGAC 472
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
121 AspProLeuAspLeuIleGlyAlaGlyAspGlnGlyLeuMetPheGlyPheAlaValAsp 140
QY 473 GAAACCCAGAAATTCATGCCATTCAGTTCATGTTCTTGCACACTAAACTCGGTGCTGCTC 532
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
141 GluThrGluGluLeuMetProLeuProIleAlaLeuSerHisLysLeuIleArgArgLeu 160
QY 533 ACCGAGGTTCCCAAGAACGGAACCTGCCATGTTTCCAGTTCGTTGCTCCACACTGTG 649
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161 AlaGluLeuArgLysSerGlyGluIleSerTyrLeuArgProAspAlaLysSerGlnVal 180
QY 593 ACTGTTGAGTAT---TACAATGACAAACGCTGCCATGTTCCAGTTCGTTGCTCCACACTGTG 649
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181 ThrValGluTyrAspGluAsnAspArg-----ProValArgValAspThrVal 196
QY 650 CTTATCTCCACCCCAACATGATGAGACTGTGACCAACGACGAAATTCGACGCTCAAG 709
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QY 710 GAGCATGTATCAAGCCGCTGATCCCGAGAGTACCTTGTATGAGAAACCATTTTCCAC 769
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217 AspLysValIleLysGluValIleProSerSerTyrLeuAspAspLysThrLysPhe 236
QY 770 TTGAACCCCTCTGGCCGTTTGTTCATTCGAGGTCTCTCACGGTGTGCTGCTCACCCGC 829
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237 IleAsnProThrGlyArgPheValIleGlyProGlnGlyAspSerGlyLeuThrGly 256
QY 830 CCGAAGATCATCATCATGATCTTACCGAGATGGGTGCTCATGGTGGTGGTCTTCTCC 889
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
257 ArgLysIleIleValAspThrTyrGlyGlyTyrSerArgHisGlyGlyGlyAlaPheSer 276
QY 890 GCGAAGGATCCCAACCAAGTTCATAGGAGTGTGCTTACATTTGTGAGCAGGCTCTCAAG 949
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
277 GlyLysAspAlaThrLysValAspArgSerAlaSerTyrAlaAlaArgTyrIleAlaLys 296
QY 950 AGCATTTGGCAAGTGGACTACCCAGAGAGTGCATTTGTGCAAGTGTCTTATGCCATTGGT 1009
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
297 AsnIleValAlaAlaGlyLeuAlaLysLysAlaGluValGlnLeuAlaTyrAlaIleGly 316
QY 1010 GTGCCCGAGCCTTGTCTGCTTTGTGACACTATGGCACCAGGAGATCCATCATGAAG 1069
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
317 ValAlaGlnProValSerValArgIleAspThrPheGlyThrGlyThrValAlaGluSer 336
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**THIS PAGE BLANK (USPTO)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model  
Run on: August 25, 2005, 17:07:17 ; Search time 228 Seconds  
(without alignments)  
5118.381 Million cell updates/sec

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
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Searched: 1767149 seqs, 392926209 residues  
Total number of hits satisfying chosen parameters: 3534298

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Database : Published Applications AA:  
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22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pcp:

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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2	2149	78.2	421	15	US-10-425-114-45874 Sequence 45874, A
3	2149	78.2	421	15	US-10-425-114-46284 Sequence 46284, A
4	2149	78.2	421	15	US-10-425-114-51724 Sequence 51724, A
5	2149	78.2	421	15	US-10-425-114-71917 Sequence 71917, A
6	2149	78.2	422	15	US-10-425-114-51415 Sequence 51415, A
7	2149	78.2	423	15	US-10-425-114-43754 Sequence 43754, A
8	2149	78.2	423	15	US-10-425-114-44216 Sequence 44216, A
9	2149	78.2	423	15	US-10-425-114-45712 Sequence 45712, A
10	2149	78.2	423	15	US-10-425-114-45723 Sequence 45723, A
11	2149	78.2	423	15	US-10-425-114-51430 Sequence 51430, A
12	2149	78.2	423	15	US-10-425-114-53617 Sequence 53617, A
13	2149	78.2	423	15	US-10-425-114-68219 Sequence 68219, A
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15	2149	78.2	423	15	US-10-425-114-71916 Sequence 71916, A
16	2149	78.2	423	15	US-10-425-114-71922 Sequence 71922, A
17	2149	78.2	423	15	US-10-425-114-71923 Sequence 71923, A
18	2149	78.2	423	15	US-10-425-114-71929 Sequence 71929, A
19	2149	78.2	423	15	US-10-425-114-71954 Sequence 71954, A
20	2149	78.2	423	15	US-10-425-114-71966 Sequence 71966, A
21	2149	78.2	423	15	US-10-425-114-71968 Sequence 71968, A
22	2149	78.2	423	15	US-10-425-114-71969 Sequence 71969, A
23	2149	78.2	423	15	US-10-425-114-71975 Sequence 71975, A
24	2149	78.2	423	15	US-10-425-114-71992 Sequence 71992, A
25	2149	78.2	423	15	US-10-425-114-71993 Sequence 71993, A
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27	2149	78.2	423	15	US-10-425-114-72190 Sequence 72190, A
28	2149	78.2	425	15	US-10-425-114-45846 Sequence 45846, A
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36	2083	75.8	392	15	US-10-424-599-220046 Sequence 220046, A
37	2083	75.8	392	16	US-10-734-698A-39 Sequence 39, Appl
38	2083	75.8	392	17	US-10-917-602A-39 Sequence 39, Appl
39	2062.5	75.1	393	15	US-10-424-599-220047 Sequence 220047, A
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42	2015.5	73.3	420	15	US-10-425-114-44746 Sequence 44746, A
43	2015.5	73.3	420	15	US-10-425-114-46219 Sequence 46219, A
44	2015.5	73.3	421	15	US-10-425-114-54713 Sequence 54713, A
45	2015.5	73.3	422	15	US-10-425-114-43848 Sequence 43848, A

ALIGNMENTS

RESULT 1  
US-10-425-114-55424  
; Sequence 55424, Application US/10425114  
; Publication No. US2004003488A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 55424  
; LENGTH: 421  
; TYPE: PRT

; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: UC-GMFLMINSOY064D01\_FLI.pep  
US-10-425-114-55424

Alignment Scores:  
Pred. No.: 5,87e-193 Length: 421  
Score: 2150.00 Matches: 410  
Percent Similarity: 97.63% Conservative: 2  
Best Local Similarity: 97.16% Mismatches: 3  
Query Match: 78.24% Indels: 7  
DB: 15 Gaps: 1

US-10-734-698A-38 (1-1485) x US-10-425-114-55424 (1-421)

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QY 4 CAAGCCCCACTCAACACACACACACT-----CTCTGCTCTTT 45
Db 1 GlnAlaProLeuAenHisThrSerProArgSerArgTyrProPhe-LeuLeuPhePh 20
QY 46 CTACCTTTCAAGTTTTTAAGTATTAAAGTGGCAGAGACATTCCTATTACCTCAGAGTC 105
Db 20 eTyrLeuSerSerPheLysSerIleLysMetAlaGluThrPheLeuPheThrSerGluSe 40
QY 106 AGTGAACGAGGACACCCCTGACAAGCTCTGCGACCAAAATCTCCGATGCTGCTCTCGAGCG 165
Db 40 rValanGluGlyHisProaspLysLeuCysaspGlnIleSerAspAlaValLeuAspAl 60
QY 166 TTGCTCTTGAACAGGCCACAGACAGCAAGGTTCCCTCGCAAAATGCACCAAGACCAACTT 225
Db 60 acYsLeuGluGlnAspProaspSerLysValAlaCySgIuThrCysThrLysThrAsnLe 80
QY 226 GGTATGCTCTTCGAGAGATCACACCAAGGCCACCTTGACTACGAGAGATCGTCGG 285
Db 80 uValMetValPheGlyGluIleThrThrLysAlaAsnValAspTyrGluLysIleValAr 100
QY 286 TGACACCTCAGGAACATCGGCTTGCTCTCAACAGATGGGACTTGATGCTGCAAACTG 345
Db 100 gasPThrCysArgAsnIleGlyPheValSerAsnaspValGlyLeuAspAlaaspAsnCy 120
QY 346 CAAGTCTCTTTAAACATTGACAGACAGACCCCTGATATGCGCCAGGGGTGACAGGCCA 405
Db 120 sLysValLeuValAsnIleGluGlnSerProaspIleAlaGlnGlyValHisGlyHi 140
QY 406 CCTTACCAAAAGACCGGGAATCGGTCTGAGACACGAGGTACATCTTTGGCTATGC 465
Db 140 sleuThrLysLysProGluGluIleGlyAlaGlyaspGlnGlyHisMetPheGlyTyrAl 160
QY 466 CACGACGAAACCCAGAAATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 525
Db 160 aThrAspGluThrProGluLeuMetProLeuSerHisValLeuAlaThrLysLeuGlyAl 180
QY 526 TCGTCTCACCGAGTTGCAAGAACGAACTGCGCCATGTTGAGCGCTGATGGGAAAC 585
Db 180 aArgLeuThrGluValArgLysAsnGlyThrCysProTyrLeuArgProaspGlyLysTh 200
QY 586 CCAAGTGACTGTGAGTATTACATGACACACCGTCGCATGTTCCAGTTCGTGTCACAC 645
Db 200 rGlnValThrValGluTyrTyrAsnAspAsnGlyAlaArgValProValArgValHisTh 220
QY 646 TGTGCTTATCTCCACCAACATGATGAGACTGTGACCAACGACGAAATTCAGCTGACCT 705
Db 220 rValLeuIleSerThrGlnHisAspGluThrValThrAsnAspGluIleAlaAspLue 240
QY 706 CAAGGAGCATGTGATCAACCGCGTGATCCCGAGAGTACCTTGATGAGAGACCACTTT 765
Db 240 uLysGluHisValIleLysProValIleProGluLysTyrLeuAspGluLysThrIlePh 260
QY 766 CCATTGACCCCTCTGGCGGTTTGTCTATTGGAGGTCTCAGCTGATGCTGGTCTCAC 825
Db 260 eHiLsLeuAsnProSerGlyArgPheValIleGlyGlyProHisGlyAspAlaGlyLeuTh 280
QY 826 CGGCGCGAAGATCATCATGATCATTCACGAGGATGGGTGCTCATGGTGGTGGTCTTT 885
```

```
Db 280 rGlyArgLysIleIleIleAspThrTyrGlyGlyTyrGlyAlaHisGlyGlyAlaph 300
QY 386 CTCGGGAGAGATCCCAACCAAGGTTGATAGAGTGGTCTTACATTGTGACACAGGCTGC 945
Db 300 eSerGlyLysAspProThrLysValAspArgSerGlyAlaTyrIleValArgGlnAlaAl 320
QY 946 TAAGAGCATTTGTGGCAAGTGGACTAGCCAGAAAGTGATTTGTGCAAGTGTCTTATGCCAT 1005
Db 320 aLysSerIleValAlaSerGlyLeuAlaArgArgCyIleValGlnValSerTyrAlaIl 340
QY 1006 TGGTGTGCCGAGCCTTTGCTGTCTTTGTGTGACACCTATGGCACCGGGAAGATCCATGA 1065
Db 340 eGlyValProGluProLeuSerValPheValAspThrTyrGlyThrGlyLysIleHisAs 360
QY 1066 TAAGCAGATTCTCAACATTGTGAAGGAACTTTGATTTCAGGCCCGGTATGATCTCCAT 1125
Db 360 pLysGluIleLeuAsnIleValLysGluAsnPheAspPheArgProGlyMetIleSerIl 380
QY 1126 CAACCTTGATCTCAAGAGGGGTGGGAATAACAGAGTTCTTGAAGACTGCTGCATATGGACA 1185
Db 380 eAsnLeuAspLeuLysArgGlyGlyAsnAsnArgPheLeuLysThrAlaAlaTyrGlyHi 400
QY 1186 CTTCGGCAGAGAGACCCCTGACTTCACATGGGAAGTGGTCAAGCCCTCAAAGTGGGAGAA 1245
Db 400 sPheGlyArgGluAspProaspPheThrTyrGluValValLysProLeuLysTyrGluLy 420
QY 1246 GGCC 1249
Db 420 sAla 421
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## RESULT 2

US-10-425-114-45874  
; Sequence 45874, Application US/10425114  
; Publication No. US20040034888A1

## GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(5313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 45874  
; LENGTH: 421  
; TYPE: PRT  
; ORGANISM: Glycine max

; FEATURE:  
; OTHER INFORMATION: Clone ID: 701001311\_FLI.pep  
US-10-425-114-45874

Alignment Scores:  
Pred. No.: 7,29e-193 Length: 421  
Score: 2149.00 Matches: 409  
Percent Similarity: 97.63% Conservative: 3  
Best Local Similarity: 96.92% Mismatches: 7  
Query Match: 78.20% Indels: 7  
DB: 15 Gaps: 1

US-10-734-698A-38 (1-1485) x US-10-425-114-45874 (1-421)

```
QY 4 CAAGCCCCACTCAACACACACACACT-----CTCTGCTCTTT 45
Db 1 GlnAlaProLeuAenHisThrSerProArgSerArgTyrProPhe-LeuLeuPhePh 20
QY 46 CTACCTTTCAAGTTTTTAAGTATTAAAGTGGCAGAGACATTCCTATTACCTCAGAGTC 105
Db 20 eTyrLeuSerSerPheLysSerIleLysMetAlaGluThrPheLeuPheThrSerGluSe 40
```





```
Db      260 eHisLeuAsnProSerGlyArgPheValIleGlyGlyProHisGlyAspAlaGlyLeuTh 280
QY      826 CGCGCCGCAAGATCATCATCTACTTACGAGAGATGGGGTCTCATGGTGGTCTCTT 885
Db      280 rGlyArgLySleIleIleAspThrTyGlyGlyTrpGlyAlaHisGlyGlyAlaPh 300
QY      886 CTCGGGAAGGATCCCAAGGTTGATAGAGTGGTGTACATTGTGAGACAGCTGC 945
Db      300 eSerGlyLyAspProThrLySValAspArgSerGlyAlaTyrIleValArgGlnAlaI 320
QY      946 TAAGACATTGTGGCAAGTGATAGCCAGAGAGTGCATTGTCAAGTCTTATGCCAT 1005
Db      320 aLySeriLeValAlaSerGlyLeuAlaArgArgCysIleValGlnValSerTyzAlaI 340
QY      1006 TGTGTGCGCCGAGCTTGTCTGTCTTTGTTCACCTATGGCACCAGGAGATCCATGA 1065
Db      340 eGlyValProGluProLeuSerValPheValAspThrTyGlyThrGlyLySleHisAs 360
QY      1066 TAAGGAGATTCTCAACATTGTGAAGGAGAACTTTGATTTTCAGCCCGGTATGATCTCCAT 1125
Db      360 pLySLeuIleLeuAsnIleValLySLeuAsnPheAspPheArgProGlyMetIleSeril 380
QY      1126 CAACCTTGATCTCAAGGGGTGGGATACAGGTTCTTGAAGACGTCTGACATATGACA 1185
Db      380 eAsnLeuAspLeuLySArgGlyGlyAsnAsnArgPheLeuLyThrAlaAlaTyrglyHi 400
QY      1186 CTTCCGACAGAGAGCCCTGACTTCACATGGGAAGTGGTCAAGCCCTCAAGTGGGAGAA 1245
Db      400 sPheGlyArgGluAspProAspPheThrTrpGluValValLySProLeuLyStrpGluLy 420
QY      1246 GGCC 1249
Db      420 sAla 421

RESULT 5
US-10-425-114-71917
; Sequence 71917, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 71917
; LENGTH: 421
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700751645_FLI.pep
US-10-425-114-71917
```

```
Alignment Scores:
Pred. No.:      7,29e-193      Length:      421
Score:          2149.00      Matches:      409
Percent Similarity: 97.63%      Conservative: 3
Best Local Similarity: 96.92%      Mismatches: 3
Query Match:      78.20%      Indels:      7
DB:              15          Gaps:      1
```

US-10-734-698A-38 (1-1485) x US-10-425-114-71917 (1-421)

```
QY      4 CAAGCCCCACTCAACACACACACCACT-----CTCTCTGCTCTTCTT 45
Db      1 GlnAlaProLeuAsnHisHisThrSerProArgSerArgTyProPhe-LeuLeuPhePh 20
```

```
QY      46 CTACCTTTCAAGTTTTTAAAGTATTAAAGATGGCAGAGACATCTCTATTTACCTCAGATC 105
Db      20 eTyrlLeuSerSerPheLySeriLeuMetAlaGluThrPheLeuPheThrSerGluSe 40
QY      106 AGTGAACAGGAGACACCTCTGACAAGCTCTGCCACCAATCTCCGATCTGCTCTCAGCG 165
Db      40 rValAsnGluGlyHisProAspLyLeuCysAspGlnIleSerAspAlaValLeuAspAl 60
QY      166 TTGCTTTGAACAGGACCCAGACAGCAAGGTTCCCTGCGAAACATGCACCAAGACCAACTT 225
Db      60 aCysLeuGluGlnAspProAspSerLySValAlaCysGluThrCysThrLySThrAsnLe 80
QY      226 GGTCTATGTTCTTCGAGAGATCACCAAGGACCAAGCTTGACTACGAGAAGATCGTGG 285
Db      80 uValMetValPheGlyGluIleThrThrLySAlaAsnValAspTyrgluLySleValAr 100
QY      286 TCACACCTGCAGAAACATCGGCTTCTCTCAACAGATGGGACTGGACTGTGCTGACAAC 345
Db      100 gAspThrCysArgAsnIleGlyPheValSerAsnAspValGlyLeuAspAlaAspAsnCy 120
QY      346 CAAGGTCTCTTGTAAACATTGAGCAGCAGAGCCCTGATATTGCCAGGGTGTGCACGGCCA 405
Db      120 sLySValLeuValAsnIleGluGlnSerProAspIleAlaGlnGlyValHisGlyHi 140
QY      406 CCTTACCAAAAGACCCGAGGAAATCGGTCTCGAGACCAAGGCTCACATGTTTGGCTATGC 465
Db      140 sLeuThrLySlySProGluGluIleGlyAlaGlyAspGlnGlyHisMetPheGlyTyraI 160
QY      466 CACGACGAAACCCAGAAATTGATGCCATTGAGTCATGTTCTTGCAACTAAACTCGGTGC 525
Db      160 aThrAspGluThrProGluLeuMetProLeuSerHisValLeuAlaThrLySLeuGlyAl 180
QY      526 TCGTCTCACCGAGGTTCCGAACCGAACCTGCCCATGGTTGAGSCCTGATGGGAAAC 585
Db      180 aArgLeuThrGluValAlaArgLySAsnGlyThrCysProIlePheUArgProAspGlyLySth 200
QY      586 CCAAGTGAATGTTGAGTATTACAATGACAAACGGTGCCTATGGTTCCAGTTTCGTGTCACAC 645
Db      200 rGlnValThrValGluTyrTyrgAsnAspAsnGlyAlaArgValProIleArgValHisTh 220
QY      646 TGTGCTTATCTCCACCAACATGATGAGACTGTGACCAACGACGAGAAATTCAGAGTGCACCT 705
Db      220 rValLeuIleSerThrGlnHisAspGluThrValThrAsnAspGluIleAlaAlaAspLe 240
QY      706 CAAGGAGCATGTGATCAAGCGGTGCATCCCGAGAGAGTACCTTGATGAGAAGACCACTTT 765
Db      240 uLySLeuHisValIleLySProValIleProGluLySlyrLeuAspGluLySThrIlePh 260
QY      766 CCACCTTGAACCCCTCTCGGCCGTTTTTGTTCATTGGAGGTCTCTACGGTGTGCTGGTCTCAC 825
Db      260 eHisLeuAsnProSerGlyArgPheValIleGlyGlyProHisGlyAspAlaGlyLeuTh 280
QY      826 CGGCGCAGATCATCATCGATACATTACGGAGGATGGGGTGTCTCATGGTGGTGGTCTTT 885
Db      280 rGlyArgLySleIleIleAspThrTyrglyGlyTrpGlyAlaHisGlyGlyGlyAlaPh 300
QY      886 CTCGGGAAGGATCCCAAGTGTGATAGGAGTGGTCTTACATTGTGAGACAGGCTGC 945
Db      300 eSerGlyLyAspProThrLySValAspArgSerGlyAlaTyrIleValArgGlnAlaI 320
QY      946 TAAGACATTGTGGCAAGTGATAGCCAGAGAGTGCATTGTGCAAGTCTTATGCCAT 1005
Db      320 aLySeriLeValAlaSerGlyLeuAlaArgArgCysIleValGlnValSerTyzAlaI 340
QY      1006 TGTGTGCGCCGAGCTTGTCTGTCTTTGTTCACCTATGGCACCAGGAGATCCATGA 1065
Db      340 eGlyValProGluProLeuSerValPheValAspThrTyrglyThrGlyLySleHisAs 360
QY      1066 TAAGGAGATTCTCAACATTGTGAAGGAGAACTTTGATTTTCAGCCCGGTATGATCTCCAT 1125
Db      360 pLySLeuIleLeuAsnIleValLySLeuAsnPheAspPheArgProGlyMetIleSeril 380
QY      1126 CAACCTTGATCTCAAGGGGTGGGAAATAACAGGTTCTTGAAGACTGTGCTGATATGACA 1185
```

```
Db 380 eAnLeuAapLeuLysArgGlyGlyAsnAsnArgPheLeuLysThrAlaAlaTyGlyHi 400
QY 1186 CTTGGCAGAGAGCCCTGACTTCAATGGAAGTGTCAAGCCCTCAAGTGGAGAA 1245
Db 400 sPheGlyArgGluAapProAapPheThrTrpGluValValLysProLeuLysTrpGluLy 420
QY 1246 GGCC 1249
Db 420 sAla 421

RESULT 6
US-10-425-114-51415
; Sequence 51415, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53113)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 51415
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700748001_FLI.pep
US-10-425-114-51415
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Alignment Scores:
Pred. No.: 7,29e-193 Length: 422
Score: 2149.00 Matches: 409
Percent Similarity: 97.63% Conservative: 3
Best Local Similarity: 96.92% Mismatches: 3
Query Match: 78.20% Indels: 7
DB: 15 Gaps: 1

US-10-734-698A-38 (1-1485) x US-10-425-114-51415 (1-422)
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QY 4 CAAGCCCCACTCAACACACACCACT-----CTCTCTGCTCTTCT 45
Db 2 GlnAlaProLeuAsnHisHisThrSerProArgSerArgTyPrPhe-LeuLeuPhePh 21
QY 46 CTACCTTTCAAGTTTAAAGTATTAAAGATGCGAGAGACATTCTCTATTACCTCAGATC 105
Db 21 eTyLeuSerSerPheLysSerIleLysMetAlaGluThrPheLeuPheThrSerGluSe 41
QY 106 AGTGAACAGGAGACCCCTGACAAGCTCTGCCACCAAACTCTCCGATGCTCTCGAGCG 165
Db 41 rValAenGluGlyHisProAapLysLeuCysAapGlnIleSerAapAlaValLeuAapAl 61
QY 166 TTGCCTTGAACAGGACCCAGACAGCAAGGTTGCCTGCGAAACATGCAACCAAGCAACTT 225
Db 61 aCysLeuGluGlnAapProAapSerLysValAlaCysGluThrCysThrLysThrAsnLe 81
QY 226 GGTCTATGTTCTCGAGAGATCACACCAAGCCCAAGTGTGACTAGGAGAAGATCGTGG 285
Db 81 uValMetValPheGlyGluLeThrThrLysAlaAsnValAapTyTrpGluLysIleValAr 101
QY 286 TGACACCTCAGGAACATCGGCTTGCTCTCAACAGATGGGACTTGTAGCTGACAACTG 345
Db 101 gAapThrCysArgAsnIleGlyPheValSerAsnAapValGlyLeuAapAlaAspAsnC 121
QY 346 CAAGGTCTTTGAAACATTGAGCAGCAGACCCCTGATTTGCCAGGGGTGTCACGGCCA 405
Db 121 sLysValLeuValAenIleGluGlnSerProAapIleAlaGlnGlyValHisGlyHi 141
```

```
QY 406 CTTTACCAAAAGACCCGAGGAATCGGTGCTGGAGACCAAGGTCACTGTTTGGCTATGC 465
Db 141 sLeuThrLysLysProGluGluIleGlyAlaGlyAspGlnGlyHisMetPheGlyTyAl 161
QY 466 CACGCAAAACCCAGAAATGATGCCATTCAGTTCATGTCCTTTCGCAACTAAACTCGGTGC 525
Db 161 aThrAapGluThrProGluLeuMetProLeuSerHisValLeuAlaThrLysLeuGlyAl 181
QY 526 TCGTCTCACGAGGTTCCAAAGAACCGCAACTGTCGCCATGTTGGTGGCCCTGATGGAAAAAC 585
Db 181 aArgLeuThrGluValArgLysAsnGlyThrCysProTrpLeuArgProAapGlyLysTh 201
QY 586 CCAAGTGACTCTTGATATTACATGACAAAGGTGCCATGGTTCAGTTCGTGTCACAC 645
Db 201 rGlnValThrValGluTyTrpAsnAapAsnGlyAlaAargValProIleArgValHisTh 221
QY 646 TGTGCTTATCTCCACCCCAACATGATGACTGTGACCAACGACCAAAATTCAGGTGACCT 705
Db 221 rValLeuIleSerThrGlnHisAapGluThrValThrAsnAapGluIleAlaAaspLe 241
QY 706 CAAGGAGCATGTGATCAAGCCGTTGATCCCGAAGAGTACCTTGATGAGAAGACCATTTT 765
Db 241 uLysGluHisValIleLysProValIleProGluLysTyLeuAaspGluLysThrIlePh 261
QY 766 CCATTGAGACCCCTCTGGCGGTTTTGTCAATTTGGAGGTCTCCACGGTGAATGCTGCTCAC 825
Db 261 eHisLeuAsnProSerGlyArgPheValIleGlyGlyProHisGlyAspAlaGlyLeuTh 281
QY 826 CGCGCGCAAGATCATCATGATCTACCGAGGATGGGGTCTCATGTGTTGGTGTCTTT 885
Db 281 rGlyArgLysIleIleIleAaspThrTyGlyGlyTrpGlyAlaHisGlyGlyAlaPh 301
QY 886 CTCCGGGAAGGATCCCAACCAAGGTGTAGAGTGGTGTCTTACATTTGTGAGACAGGCTGC 945
Db 301 eSerGlyLysAapProThrLysValAapArgSerGlyAlaTyIleValAargGlnAlaAl 321
QY 946 TAAGAGCATTTCTGGCAGTGAAGTACGAGAGGTGCATTTGCAAGTGTCTTATGCCAT 1005
Db 321 aLysSerIleValAlaSerGlyLeuAlaAargCysIleValGlnValSerTyAlaAl 341
QY 1006 TGGTGTGCCCGAGGCTTTGTCTGCTTTTGTGACACCTTATGGCACCGGGAAGATCCATGA 1065
Db 341 eGlyValProGluProLeuSerValPheValAapThrTyrcGlyThrGlyLysIleHisAs 361
QY 1066 TAAGAGATTCTCAACATTGTGAAGGAGAACTTTGATTTTACGGCCCGGTATGATCTCAT 1125
Db 361 pLysGluIleLeuAsnIleValLysGluAsnPheAapPheArgProGlyMetIleSerIl 381
QY 1126 CAACCTTGATCTCAAGAGGGGTGGGAATAACAGGTTCTTTGAAGACTGCTGCATATGGACA 1185
Db 381 eAsnLeuAapLeuLysArgGlyGlyAsnAsnArgPheLeuLysThrAlaAlaTyGlyHi 401
QY 1186 CTTCCGACAGAGAGACCCCTGACTTTCACATGCGAAAGTGTGCAAGCCCTCAAGTGGAGAA 1245
Db 401 sPheGlyArgGluAapProAapPheThrTrpGluValValLysProLeuLysTrpGluLy 421
QY 1246 GGCC 1249
Db 421 sAla 422
```

## RESULT 7

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US-10-425-114-43754
; Sequence 43754, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
```



; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 43754  
; LENGTH: 423  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700654923\_FLI.pep  
US-10-425-114-43754

## Alignment Scores:

Pred. No.: 7,3e-193 Length: 423  
Score: 2149.00 Matches: 409  
Percent Similarity: 97.63% Conservatives: 3  
Best Local Similarity: 96.92% Mismatches: 3  
Query Match: 78.20% Indels: 7  
DB: 15 Gaps: 1

US-10-734-698A-38 (1-1485) x US-10-425-114-43754 (1-423)

QY 4 CAGCCCTCACTCAACACACACACT-----CTCTCTGCTCTTCT 45  
DB 3 GlnAlaProLeuAsnHisThrSerProArgSerArgTyrProPhe-LeuLeuPhePh 22  
QY 46 CTACCTTTCAAGTTTAAAGTATTAAAGATGGCAGAGACATCTCTATTACCTTCACAGTC 105  
DB 22 eTyrLeuSerSerPheLysSerLysMetAlaGluThrPheLeuPheThrSerGluSe 42  
QY 106 AGTGAACGAGGGACACCCCTGACAACTCTCGACACCAAACTCTCGATGCTGCTCGACGC 165  
DB 42 rValAsnGluGlyHisProAspLysLeuCysAspGlnIleSerAspAlaValLeuAspAl 62  
QY 166 TTGCTTTGAACAGGACCCAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 225  
DB 62 aCysLeuGluGlnAspProAspSerLysValAlaCysGluThrCysThrLysThrAsnLe 82  
QY 226 GGTCTATGCTTCGGAGAGATCACCAAGGCGCAAGCTTGACTACGAGAGATCGTGC 285  
DB 82 uValMetValPheGlyGluIleThrThrLysAlaAsnValAspTyrGluLysIleValAr 102  
QY 286 TGACACCTGTCAGGAACATCGCTCTCTCAACAGATGGGAGATTCGATGCTGACAACTG 345  
DB 102 gaepThrCysArgAsnIleGlyPheValSerAsnAspValGlyLeuAspAlaAspAsnCy 122  
QY 346 CAAGGTCCTTGTAAACATTGAGCAGCAGAGCCCTGATATTGCCAGGGTGTGCACGGCCA 405  
DB 122 sLysValLeuValAsnIleGluGlnGlnSerProAspIleAlaGlnGlyValHisGlyHi 142  
QY 406 CCTTACCAAGAACCCGAGGAATCGTCTGAGACCCAGGGTCACATGTTTGGCTATGC 465  
DB 142 sleuThrLysLysProGluGluIleGlyAlaGlyAspGlnGlyHisMetPheGlyTyrAl 162  
QY 466 CAGGACGAAACCCCAAGAAATGATGCAATGATGATGCTTCTGCAACTAAATCCGGTGC 525  
DB 162 aThrAspGluThrProGluLeuMetProLeuSerHisValLeuAlaThrLysLeuGlyAl 182  
QY 526 TCGTCTCACCAGGTTGCGAAGAACCGGAACCTGCCCATGTTGAGCCCTGATGGGAAAC 585  
DB 182 aArgLeuThrGluValArgLysAsnGlyThrCysProTrpLeuArgProAspGlyLysTh 202  
QY 586 CCAAGTGACTGTGAGTATTACATACACACGTCGATGCTTCCAGTTCGTGTCACAC 645  
DB 202 rGlnValThrValGluTyrTyrAsnAspAsnGlyAlaArgValProIleArgValHisTh 222  
QY 646 TGTGCTTATCTCCACCAACATGATGAGACTGTGACCAACGACGAAATTCGACGTCACCT 705  
DB 222 rValLeuIleSerThrGlnHisAspGluThrValThrAsnAspGluIleAlaAlaAspLe 242  
QY 706 CAAGGACGATGATCAAGCCGCTGATCCCGGAGAGTACCTTGTATGAGAACCACTTTT 765

DB 242 ulysGluHisValIleLysProValIleProGluLysTyrLeuAspGluLysThrIlePh 262  
QY 766 CCACCTTGAAACCCCTCTGGCCGCTTTTGTTCATTGGAGGTCTCTACGGTGATGCTGCTCAC 825  
DB 262 ehIsLeuAsnProSerGlyArgPheValIleGlyGlyProHisGlyAspAlaGlyLeuTh 282  
QY 826 CGGCCCAAGATCATCATCATCTTACCGAGAGATGGGTGCTCATGGTGGTGGTCTTT 885  
DB 282 rGlyArgLysIleIleIleAspThrTyrGlyTrpGlyAlaHisGlyGlyGlyAlaPh 302  
QY 886 CTCGGGAGAGATCCCAACAGGTTGATAGGAGTGGTCTTACATTGTGACAGACGCTGC 945  
DB 302 eSerGlyLysAspProThrLysValAspArgSerGlyAlaIleValArgGlnAlaAl 322  
QY 946 TAAGAGCATTTGTGCAAGTGGACTAGCCAGAAAGTGCATTGTGCAAGTCTCTTATGCCAT 1005  
DB 322 alysserIleValAlaSerGlyLeuAlaArgArgCysIleValGlnValSerTyrAlaAl 342  
QY 1006 TGGTGTGCCGAGCCTTTGCTCTTGTGTTGACACCTATGGCACCGGGAAGATCCATGA 1065  
DB 342 eGlyValProGluProLeuSerValPheValAspThrTyrGlyThrGlyLysIleHisAs 362  
QY 1066 TAAGAGCATTTCTCAACATTTGGAAGGAGAACTTTCATTTCAGGCCGGTATGATCTCCAT 1125  
DB 362 physGluIleLeuAsnIleValLysGluAsnPheAspPheArgProGlyMetIleSerIl 382  
QY 1126 CAACCTTGATCTCAAGAGGGTGGGAATAACAAGGTTCTTGAAGACTGCTGCATATGGACA 1185  
DB 382 eAsnLeuAspLeuLysArgGlyGlyAsnAsnArgPheLeuLysThrAlaAlaTyrGlyHi 402  
QY 1186 CTTCCGACAGAGAGACCTCTGACTTCAATGGGAAGTGTGCAAGCCCTCAAGTGGGAGAA 1245  
DB 402 sPheGlyArgGluAspProAspPheThrTrpGluValLysProLeuLysTrpGluLys 422  
QY 1246 GSCC 1249  
DB 422 sAla 423

## RESULT 8

US-10-425-114-44216  
; Sequence 44216, Application US/10425114  
; Publication NO. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E.  
; APPLICANT: Tabaska, Jack E.  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 44216  
; LENGTH: 423  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700901925\_FLI.pep  
US-10-425-114-44216

## Alignment Scores:

Pred. No.: 7,3e-193 Length: 423  
Score: 2149.00 Matches: 409  
Percent Similarity: 97.63% Conservatives: 3  
Best Local Similarity: 96.92% Mismatches: 3  
Query Match: 78.20% Indels: 7  
DB: 15 Gaps: 1

US-10-734-698A-38 (1-1485) x US-10-425-114-44216 (1-423)



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QY 4 CAAGCCCCACTCAACACACACCACT-----CTCTCTCTCTCTT 45
Db 3 GlnAlaProLeuAsnHisThrSerProArgSerArgTyrProPhe-LeuLeuPhePh 22
QY 46 CTACCTTTCAAGTTTAAAGATTAAAGATGCGAGAGACATTCCCTATTATTCCTCAGAGTC 105
Db 22 eTyrLeuSerSerPheLysSerIleLysMetAlaGluThrPheLeuPheThrSerGluSe 42
QY 106 AGTGAACGAGGACACCCCTGACAACTCTGCAACCAATCTCCGATCTGCTCTCGAGCC 165
Db 42 rValAsnGluGlyHisProAspLysLeuCysAspGlnIleSerAspAlaValLeuAspAl 62
QY 166 TTGCTTTGAACAGGACCCAGACAGCAAGCTTGCTCGCAAAACATGCAACAGCAACTT 225
Db 62 aCysLeuGluGlnAspProAspSerLysValAlaCysGluThrCysThrLysThrAsnLe 82
QY 226 GGTCTATGCTTCGGAGAGATCACCAAGGCGCAACGTTGACTACGAGAAGATCGTGG 285
Db 82 uValMetValPheGlyGluIleThrThrLysAlaAsnValAspTyrGluLysIleValAr 102
QY 286 TGACACCTCAGGAACATCGGCTTCGCTCAACAGTGGGACTTGAGCTGCAACTG 345
Db 102 gAspThrCysArgAsnIleGlyPheValSerAsnAspValGlyLeuAspAlaAspAsnCy 122
QY 346 CAAGGTCCTTGTAAACATTGAGCAGCAGAGCCCTGATATTGCCAGGGTGTGCAGGCCA 405
Db 122 sLysValLeuValAsnIleGluGlnGlnSerProAspIleAlaGlnGlyValHisGlyHi 142
QY 406 CTTTACCAAAGACCCGAGAAATCGGTCTCGAGACCAAGGTCAATGTTTGGGTATGC 465
Db 142 sLeuThrLysLysProGluGluIleGlyAlaGlyAspGlnGlyHisMetPheGlyTyrAl 162
QY 466 CAGGACGAAACCCCAAGATTGATGCCATTGATGATCTTCTGCAACTAAACTCGGTGC 525
Db 162 aThrAspGluThrProGluLeuMetProLeuSerHisValLeuAlaThrLysLeuGlyAl 182
QY 526 TCGTCTCACCGAGTTCGCAAGAACCTGCCATCGTTCGAGCCCTGATGGGAAAC 585
Db 182 aArgLeuThrGluValArgLysAsnGlyThrCysProThrLeuArgProAspGlyLysTh 202
QY 586 CCAAGTGACTGTGAGTATTACAATGACAAACGGTGCCATGGTTCAGTTTCGTGTCACAC 645
Db 202 rGlnValThrValGluTyr-TyrAsnAspAsnGlyAlaArgValProIleArgValHisTh 222
QY 646 TGTGCTATCTCCACCAACATGATGAGACTGTGACCAACGACGAATTCGAGCTGACCT 705
Db 222 rValLeuIleSerThrGlnHisAspGluThrValThrAsnAspGluIleAlaAlaAspLe 242
QY 706 CAAGGAGCATGTGATCAAGCCGCTGATCCCGAGAGTACCTTGATGAGAAGACCATTTT 765
Db 242 uLysGluHisValIleLysProValIleProGluLysTyrLeuAspGluLysThrIlePh 262
QY 766 CCACTTGAACCCCTCTGGCCGTTTGTTCATTGAGAGTCTCTACGGTGATGCTGGTCTCAC 825
Db 262 eHisLeuAsnProSerGlyArgPheValIleGlyGlyProHisGlyAspAlaGlyLeuTh 282
QY 826 CGGCCGACATCATCATCATCTTACCGAGATGGGTGCTCATGGTGGTGGTCTTT 885
Db 282 rGlyArgLysIleIleIleAspThrTyrGlyGlyTrpGlyAlaHisGlyGlyGlyAlaPh 302
QY 886 CTCGGGAAGGATCCCAACCAAGTTGATAGGAGTGGTGTCTACATTGTGAGACAGCTGC 945
Db 302 eSerGlyLysAspProThrLysValAspArgSerGlyAlaTyrIleValArgGlnAlaAl 322
QY 946 TAAGAGCATTTGGCAAGTGGACTAGCCAGAAAGGTGCATTTGCAAGTGTCTTATGCCAT 1005
Db 322 aLysSerIleValAlaSerGlyLeuAlaArgCysIleValGlnValSerTyrAlaIle 342
QY 1006 TGGTGTGCCCGACCTTCTGCTCTTGTTCACACCTATGCGACCGGGAAGATCCATCA 1065
Db 342 eGlyValProGluProLeuSerValPheValAspThrTyrGlyThrGlyLysIleHisAs 362
QY 1066 TAAGGAGATTCTCAACATTGTGAAGGAGAACTTTTGATTTTCAGGCCCGGTATGATCTCCAT 1125
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Db 362 pLysGluIleLeuAsnIleValLysGluAsnPheAspPheArgProGlyMetIleSerIl 382
QY 1126 CAACCTTGATCTCAAGAGGGGTGGGAATAACAGAGTTCTTGAAGACTGCTGCATATGGACA 1185
Db 382 eAsnLeuAspLeuLysArgGlyGlyAsnAsnArgPheLeuLysThrAlaAlaTyrGlyHi 402
QY 1186 CTTGGCAGAGAGACCCCTGACTTCACATGGGAAGTGGTCAAGCCCTCAAGTGGGACAA 1245
Db 402 sPheGlyArgGluAspProAspPheThrTrpGluValValLysProLeuLysTrpGluLy 422
QY 1246 GGCC 1249
Db 422 sAla 423
RESULT 9
US-10-425-114-45712
; Sequence 45712, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 45712
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700891875_F11.pep
US-10-425-114-45712
Alignment Scores:
Pred. No.: 7,3e-193 Length: 423
Score: 2149.00 Matches: 409
Percent Similarity: 97.63% Conservative: 3
Best Local Similarity: 96.92% Mismatches: 3
Query Match: 78.20% Indels: 7
DB: 15 Gaps: 1
US-10-734-698A-38 (1-1485) x US-10-425-114-45712 (1-423)
QY 4 CAAGCCCCACTCAACACACCACT-----CTCTCTCTCTCTT 45
Db 3 GlnAlaProLeuAsnHisThrSerProArgSerArgTyrProPhe-LeuLeuPhePh 22
QY 46 CTACCTTTCAAGTTTAAAGATTAAAGATGCGAGAGACATTCCCTATTATTCCTCAGAGTC 105
Db 22 eTyrLeuSerSerPheLysSerIleLysMetAlaGluThrPheLeuPheThrSerGluSe 42
QY 106 AGTGAACGAGGACACCCCTGACAACTCTGCAACCAATCTCCGATCTGCTCTCGAGCC 165
Db 42 rValAsnGluGlyHisProAspLysLeuCysAspGlnIleSerAspAlaValLeuAspAl 62
QY 166 TTGCTTTGAACAGGACCCAGACAGCAAGCTTGCTCGCAAAACATGCAACAGCAACTT 225
Db 62 aCysLeuGluGlnAspProAspSerLysValAlaCysGluThrCysThrLysThrAsnLe 82
QY 226 GGTCTATGCTTCGGAGAGATCACCAAGGCGCAACGTTGACTACGAGAAGATCGTGG 285
Db 82 uValMetValPheGlyGluIleThrThrLysAlaAsnValAspTyrGluLysIleValAr 102
QY 286 TGACACCTCAGGAAACATCGGCTTCGCTCAACAGTGGGACTTGAGCTGCAACTG 345
Db 102 gAspThrCysArgAsnIleGlyPheValSerAsnAspValGlyLeuAspAlaAspAsnCy 122
```

```
QY 346 CAAGGTCCTTGTAAACATTGAGCAGCAGACCCCTGTATTTGCCAGGGTGTGCACGGCCA 405
Db 122 sLysValLeuValAenIleGluGlnSerProAspIleAlaGlnGlyValHisGlyHi 142
QY 406 CTTTACCAAGACCCGAGGAATCCGTCGTGAGACCCAGGTCACATGTTGGCTATGC 465
Db 142 sLeuThrLysLysProGluGluIleGlyAlaGlyAspGlnGlyHisMetPheGlyTyrAl 162
QY 466 CACGACGAAACCCCAAGAAATGTATGTCATTCAGTTCATGTTCTTGCAACTAAACTCGGTGC 525
Db 162 aThrAspGluThrProGluLeuMetProLeuSerHisValLeuAlaThrLysLeuGlyAl 182
QY 526 TCCTCTCACCGAGTTCCGAAGAACCGAACTCCCATGTTGAGCCCTGATGGGAAAC 585
Db 182 aArgLeuThrGluValArgLysAenGlyThrCysProTrpLeuArgProAspGlyLysTh 202
QY 586 CCAAGTGACTGTTGAGTATTACATGACACGCTGCCATGTTCCAGTTCGTGTCACAC 645
Db 202 rGlnValThrValGluTyrTrpAenAspAenGlyAlaArgValProIleArgValHisTh 222
QY 646 TGTGCTTATCTCCACCAACATGATGAGCTGTGACCAACGACGAAATTCAGCTGACCT 705
Db 222 rValLeuIleSerThrGlnHisaspGluThrValThrAenAspGluIleAlaAspLe 242
QY 706 CAAGGAGCATGTGATCAAGCCGCTGATCCCGGAGAGTACCTTTGATGAGAAGACCATTTT 765
Db 242 uLysGluHisValIleLysProValIleProGluLysTyrLeuAspGluLysThrIlePh 262
QY 766 CCACTTGAAACCCCTCGCCGCTTGTCTATTGAGGTCTCAGCGTATGCTGGTCTCAC 825
Db 262 eHisLeuAenProSerGlyArgPheValIleGlyGlyProHisGlyAspAlaGlyLeuth 282
QY 826 CGGCCCAAGATCATCATCACTACTACGAGATGGGGTCTCATGGTGGTGGTCTTT 885
Db 282 rGlyArgLysIleIleIleaspThrTyrGlyGlyTrpGlyAlaHisGlyGlyAlaPh 302
QY 886 CTCGGGAAGGATCCCAAGGTTGATAGGAGTGTGCTTACATTTGTGAGACAGGCTGC 945
Db 302 eSerGlyLysAspProThrLysValAspArgSerGlyAlaTyrIleValArgGlnAlaI 322
QY 946 TAAGACATGTGGCAAGTGGACTACCGAGAGTGCATGTCAGTGTCTTATGCCAT 1005
Db 322 aLysSerIleValAlaSerGlyLeuAlaArgCysIleValGlnValSerTyrAlaI 342
QY 1006 TGTGTGCCGAGCCTTGTCTGTCTTGTGTGACCTATGACCGCGGAAGATCCATCA 1065
Db 342 eGlyValProGluProLeuSerValPheValAspThrTyrGlyThrGlyLysIleHisB 362
QY 1066 TAAGGAGATTCTCAACATTTGTAAGGAGAACTTTGATTTTCAAGCCCGGTATGATCTCCAT 1125
Db 362 pLysGluIleLeuAenIleValLysGluAenPheAspPheArgProGlyMetIleSerI 382
QY 1126 CAACCTTGATCTCAAGAGGGTGGGAATACAGGTTCTTGAGACGTGCTGCATATGGACA 1185
Db 382 eAenLeuAspLeuLysArgGlyGlyAsnAsnArgPheLeuLysThrAlaAlaTyrGlyHi 402
QY 1186 CTTCCGACAGAGGACCCCTGACTTCACATGGGAAGTGTCAAGCCCTCAAGTGGAGAA 1245
Db 402 sPheGlyArgGluAspProAspPheThrTrpGluValLysProLeuLysTrpGluL 422
QY 1246 GGCC 1249
Db 422 sAla 423
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RESULT 10

US-10-425-114-45723  
; Sequence 45723, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.

; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; NUMBER OF SEQ ID NOS: 2003-04-28  
; SEQ ID NO 45723  
; LENGTH: 423  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700896016\_FLI.pep  
US-10-425-114-45723

Alignment Scores:  
Pred. No.: 7,3e-193 Length: 423  
Score: 2149.00 Matches: 409  
Percent Similarity: 97.63% Conservative: 3  
Best Local Similarity: 96.92% Mismatches: 3  
Query Match: 78.20% Indels: 7  
DB: 15 Gaps: 1

US-10-734-698A-38 (1-1485) x US-10-425-114-45723 (1-423)

```
QY 4 CAAGCCCACTCAACACCCACACCACT-----CTCTCTGCTCTTCT 45
Db 3 GlnAlaProLeuAenHisThrSerProArgSerArgTyrProPhe-LeuLeuPhePh 22
QY 46 CTACCTTCAAGTTTTTAAAGTATTAAAGTATGAGTGGCAGAGACATTCTTATTTACCTCAGAGTC 105
Db 22 eTyrLeuSerSerPheLysSerIleLysMetAlaGluThrPheLeuPheThrSerGluSe 42
QY 106 AGTGAACGAGGACACCTTGACAAAGCTCTCGACCAAAATCTCCGATCTGCTCTCGACGC 165
Db 42 rValAsnGluGlyHisProAspLysLeuCysAspGlnIleSerAspAlaValLeuAspAl 62
QY 166 TTGCTCTGAACAGGACCCAGACAGCAGCAAGTTCTCCGCAAAACATGCACCAAGACCAACTT 225
Db 62 aCysLeuGluGlnAspProAspSerLysValAlaCysGluThrCysThrLysThrAsnLe 82
QY 226 GGTCTATGTTCTTCGAGAGATCACCACCAAGGCCAACGTTGACTACGAGAAGATCGTGG 285
Db 82 uValMetValPheGlyGluIleThrThrLysAlaAsnValAspTyrGluLysIleValAr 102
QY 286 TGACACCTGCGAGGAACATCGGCTTCGTCTCAAAACGATGTGGGACTTGATGCTGACAACTG 345
Db 102 gAspThrCysArgAenIleGlyPheValSerAsnAspValGlyLeuAspAlaAspAenCy 122
QY 346 CAAGTCTCTTGTAAACATTGAGCAGCAGCCCTCATATTGCCAGGGTGTGCACGGCCA 405
Db 122 sLysValLeuValAenIleGluGlnGlnSerProAspIleAlaGlnGlyValHisGlyHi 142
QY 406 CTTTACCAAGACCCGAGGAATCGTGTGTCGAGACCCAGGTCACATGTTTGGCTATGC 465
Db 142 sLeuThrLysLysProGluGluIleGlyAlaGlyAspGlnGlyHisMetPheGlyTyrAl 162
QY 466 CACGACGAAACCCCAAGAAATGTATGTCATTCAGTTCATGTTCTTGCAACTAAACTCGGTGC 525
Db 162 aThrAspGluThrProGluLeuMetProLeuSerHisValLeuAlaThrLysLeuGlyAl 182
QY 526 TCGTCTCACCGAGTTCCGAAGAACCGAACTCCCATGTTGAGCCCTGATGGGAAAC 585
Db 182 aArgLeuThrGluValArgLysAenGlyThrCysProTrpLeuArgProAspGlyLysTh 202
QY 586 CCAAGTGACTGTTGAGTATTACATGACACGCTGCCATGTTCCAGTTCGTGTCACAC 645
Db 202 rGlnValThrValGluTyrTrpAenAspAenGlyAlaArgValProIleArgValHisTh 222
QY 646 TGTGCTTATCTCCACCAACATGATGAGCTGTGACCAACGACGAAATTCAGCTGACCT 705
Db 222 rValLeuIleSerThrGlnHisaspGluThrValThrAenAspGluIleAlaAspLe 242
```

Db 222 rValLeuIleSerThrGlnHisAspGluThrValThrAsnAspGluIleAlaAspLe 242  
Qy 706 CAAGGAGCATGATCAACCCGGTGATCCCGAGAGTACCTTGATGAGAACCATTTT 765  
Db 242 uLysGluHisValIleLysProValIleProGluLysTyrLeuAspGluLysThrIlePh 262  
Qy 766 CCACTTGAACCCCTCGGCCGTTTGTCTCATTTGAGGTCTCACGGTGATGCTGGTCTCAC 825  
Db 262 eHisLeuAsnProSerGlyArgPheValIleGlyGlyProHisGlyAspAlaGlyLeuTh 282  
Qy 826 CGGCGCAAGATCATCATCATCTTACGAGGATGGGTGCTCATGGTGGTGGTCTTT 885  
Db 282 rGlyArgLysIleIleIleAspThrTyrGlyGlyTrpGlyAlaHisGlyGlyAlaPh 302  
Qy 886 CTCCGGGAAGGATCCACCAAGTTGATAGGAGTGGTGTCTTACATTTGAGACAGCTGC 945  
Db 302 eSerGlyLysAspProThrLysValAspArgSerGlyAlaTyrIleValArgGlnAla 322  
Qy 946 TAAGAGCATTTGGCAAGTGGACTAGCCAGAAAGTGCATTGTGCAAGTCTTATGCCAT 1005  
Db 322 aLysSerIleValAlaSerGlyLeuAlaArgCysIleValGlnValSerTyrAla 342  
Qy 1006 TGGTGTGCCGAGCCCTTGTCTGTCTTGTGTCACACCTATGGCACCGGGAAGATCCATGA 1065  
Db 342 eGlyValProGluProLeuSerValPheValAspThrTyrGlyThrGlyLysIleHis 362  
Qy 1066 TAAGGAGATCTCAACATTTGTAAGGAGAACCTTTGATTTACAGCCGGTATGATCTCCAT 1125  
Db 362 pLysGluIleLeuAsnIleValLysGluAsnPheArgPheArgProGlyMetIleSerI 382  
Qy 1126 CAACCTTGTATCTCAAGAGGGTGGGAATAACAGGTCTTGAAGACTGCTGCATATGGACA 1185  
Db 382 eAsnLeuAspLeuLysArgGlyGlyAsnAsnArgPheLeuLysThrAlaAlaTyrGly 402  
Qy 1186 CTTCGCGCAGAGAGGACCCCTGACTTCCATGGAAGTGGTCAAGCCCTCAAGTGGAGAA 1245  
Db 402 sPheGlyArgGluAspProAspPheThrTrpGluValLysProLeuLysTrpGlu 422  
Qy 1246 GGCC 1249  
Db 422 sAla 423

## RESULT 11

US-10-425-114-51430  
; Sequence 51430, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaka, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21 (5313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 51430  
; LENGTH: 423  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700901534\_FLI.pep  
US-10-425-114-51430

Alignment Scores:  
Pred. No.: 7.3e-193 Length: 423  
Score: 2149.00 Matches: 409  
Percent Similarity: 97.63% Conservative: 3  
Best Local Similarity: 96.92% Mismatches: 3  
Query Match: 78.20% Indels: 7

DB: 15 Gaps: 1  
US-10-734-698A-38 (1-1485) x US-10-425-114-51430 (1-423)  
Qy 4 CAAGCCCCACTCAACCCACCACCAACCACT-----CTCTCTGCTCTTCTT 45  
Db 3 GlnAlaProLeuAsnHisThrSerProArgSerArgTyrProPhe-LeuLeuPhePh 22  
Qy 46 CTACTTTCAAGTATTTAAAGTATTAGATGGCAGAGACATTTCTATTACTCAGAGTC 105  
Db 22 eTyrLeuSerSerPheLysSerIleLysMetAlaGluThrPheLeuPheThrSerGluSe 42  
Qy 106 AGTGAACGAGGACACCCCTGACAAAGCTCTGCGACCAAAATCTCCGATGCTGCTCGACGC 165  
Db 42 rValAsnGluGlyHisProAspLysLeuLysAspGlnIleSerAspAlaValLeuAspAl 62  
Qy 166 TTGCTTTGAACAGGACCCAGACAGCAAGTTGCTTGGGAAACATGCAACAGACCAACTT 225  
Db 62 aCysLeuGluGlnAspProAspSerLysValAlaCysGluThrCysThrLysThrAsnLe 82  
Qy 226 GGTCAATGCTCTCGAGAGATCACCAACGCGCAACGTTGACTACGAGAGATCGTGG 285  
Db 82 uValMetValPheGlyGluIleThrThrLysAlaAsnValAspTyrGluLysIleValAr 102  
Qy 286 TGACACCTGCGAGGAACATCGGCTTCTCAACGATGTGGGACTTGATGCTGCAACATG 345  
Db 102 gAspThrCysArgAsnIleGlyPheValSerAsnAspValGlyLeuAspAlaAspAsnCy 122  
Qy 346 CAAGGCTCTTTAAACATTTGAGACAGACGCTGATATTGCTCCAGGGTGTGCGGCGCA 405  
Db 122 sLysValLeuValAsnIleGluGlnGlnSerProAspIleAlaGlnGlyValHisGly 142  
Qy 406 CTTTACCAAAAGACCCGAGGAATCGGTCTGCGAGACCGGGTCACATGTTGCTGCTATGC 465  
Db 142 sLeuThrLysLysProGluGluIleGlyAlaGlyAspGlnGlyHisMetPheGlyTyrAl 162  
Qy 466 CACGCGAAACCCAGAAATGATGCCATTCAGTTCATGTCGCAACTAAACCTCGGTGC 525  
Db 162 aThrAspGluThrProGluLeuMetProLeuSerHisValLeuAlaThrLysLeuGlyAl 182  
Qy 526 TCCTCTCACCGAGTTGCGAAAGACCTGCGCAACCTGCTGAGGCTGTGAGGAAAC 585  
Db 182 aArgLeuThrGluValArgLysAsnGlyThrCysProTrpLeuArgProAspGlyLysTh 202  
Qy 586 CCAAGTGACTCTTGATGATTAACAATGACAAAGGTGCCATGCTCCAGTTCGTCACAC 645  
Db 202 rGlnValThrValGluTyrTyrAsnAspAsnGlyAlaArgValProIleArgValHisTh 222  
Qy 646 TGTCTTATCTCCACCCCAACATGATGACTGTGACCAACGACGAAATTCAGCTGACCT 705  
Db 222 rValLeuIleSerThrGlnHisAspGluThrValThrAsnAspGluIleAlaAspLe 242  
Qy 706 CAAGGAGCATGTGATCAAGCCGTTGATCCCGAGAGTACCTTGTATGAGAGACCATTTT 765  
Db 242 uLysGluHisValIleLysProValIleProGluLysTyrLeuAspGluLysThrIlePh 262  
Qy 766 CCATTTGAACCCCTCGCCGTTTGTTCATTTGGAGGTCTCTCACGGTGTGCTGCTCAC 825  
Db 262 eHisLeuAsnProSerGlyArgPheValIleGlyGlyProHisGlyAspAlaGlyLeuTh 282  
Qy 826 CGGCGCAAGATCATCATCATCTTACGAGGATGGGTGCTCATGGTGGTGGTCTTT 885  
Db 282 rGlyArgLysIleIleIleAspThrTyrGlyGlyTrpGlyAlaHisGlyGlyAlaPh 302  
Qy 886 CTCCGGGAAGGATCCACCAAGTTGATGAGGTGGTCTTACATTTGAGACAGGCTGC 945  
Db 302 eSerGlyLysAspProThrLysValAspArgSerGlyAlaTyrIleValArgGlnAla 322  
Qy 946 TAAGAGCATTTGGCAAGTGGACTAGCCAGAGGTCATTTGCAAGTCTTATGCCAT 1005  
Db 322 aLysSerIleValAlaSerGlyLeuAlaArgCysIleValGlnValSerTyrAla 342  
Qy 1006 TGGTGTGCCGAGCCCTTGTCTGTCTTGTGTCACACCTATGGCACCGGGAAGATCCATGA 1065



```
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 68219
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700757167_FLI.pbp
US-10-425-114-68219

Alignment Scores:
Pred. No.: 7,3e-193 Length: 423
Score: 2149.00 Matches: 409
Percent Similarity: 97.63% Conservative: 3
Best Local Similarity: 96.92% Mismatches: 3
Query Match: 78.20% Indels: 7
DB: 15 Gaps: 1

US-10-734-698A-38 (1-1485) x US-10-425-114-68219 (1-423)

QY 4 CAAGCCCACTCAACACACACCACT-----CTCTCTCTCTTT 45
Db 3 GlnAlaProLeuAsnHisThrSerProArgSerArgTyrProPhe-LeuLeuPhePh 22
QY 46 CTACCTTTCAAGTTTAAAGATTAAAGATGCGAGACATCTTATTACCTCAGAGTC 105
Db 22 eTyrLeuSerSerPheLysSerIleLysMetAlaGluThrPheLeuPheThrSer-GluSe 42
QY 106 AGTGAACGAGGACACCTCGA CAAGCTCTGCGACCAAAATCTCCGATGCTGCTCGAGC 165
Db 42 rValAenGluGlyHisProAspLysLeuCysAspGlnIleSerAspAlaValLeuAspAl 62
QY 166 TTGCTTTGAACAGGACCCAGACGACGAGTTCCTCGGAAACATGCACCAAGACCACTT 225
Db 62 aCysLeuGluGlnAspProAspSerLysValAlaCysGluThrCysThrLysThrAsnLe 82
QY 226 GGTCTAGTGTCTCGAGAGATCACCACCAAGCGCAACGTTGACTACGAGAAGATCGTGG 285
Db 82 uValMetValPheGlyGluIleThrThrLysAlaAenValAspTyrGluLysIleValAr 102
QY 286 TGACACCTCGAGAACATCGGCTTCGTCTCAACGATGCGGACTTGATGCTGACAACTG 345
Db 102 gaSPThrCysArgAenIleGlyPheValSerAenAspValGlyLeuAspAlaAspAenCy 122
QY 346 CAAGTCTCTTAAACATTGACGACGACGACCCCTGATATTGGCCAGGCTGTCACGGCA 405
Db 122 sLysValLeuValAenIleGluGlnSerProAspIleAlaGlnGlyValHisGlyHi 142
QY 406 CTTTACCAAAAGACCCGAGAAATCGGTGCTGAGACACGAGGTTCACATGTTGGCTATGC 465
Db 142 sleuthrLysLysProGluGluIleGlyAlaGlyAspGlnGlyHisMetPheGlyTyrAl 162
QY 466 CACGGAAGAAACCCCAAGATTGATGCCATTGATGATGATGATGATGATGATGATGATG 525
Db 162 aThrAspGluThrProGluLeuMetProLeuSerHisValLeuAlaThrLysLeuGlyAl 182
QY 526 TGGTCTCACCGAGGTTCCGAAGACCGACCTGCCCTGTTGAGCCCTGATGCGGAAC 585
Db 182 aArgLeuThrGluValArgLysAsnGlyThrCysProTrpLeuArgProAspGlyLysTh 202
QY 586 CCAAGTACTGTTGAGTATTACAAATGACACCGTGCATGTTCCAGTTCGTGTCACAC 645
Db 182 aArgLeuThrGluValArgLysAsnGlyThrCysProTrpLeuArgProAspGlyLysTh 202
```

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Db 202 rGlnValThrValGluTyrTyrAsnAspAsnGlnValAlaArgValProIleArgValHisTh 222
QY 646 TGTCTTATCTCCACCCAAACATGATGAGACTGTGACCAACGACCAAAATTGAGGTGACCT 705
Db 222 rValLeuIleSerThrGlnHisAspGluThrValThrAsnAspGluIleAlaAlaAspLe 242
QY 706 CAAGCAGCATGTGATCAAGCCGGTGATCCCGAGAAAGTACCTTGATGAGAAAGACCATTTT 765
Db 242 uLysGluHisValIleLysProValIleProGluLysTyrLeuAspGluLysThrIlePh 262
QY 766 CCATTCAACCCCTCTGGCCGCTTTTTCATTGGAGGCTCTCACGGTGTGATGCTGCTCAC 825
Db 262 eHisLeuAenProSerGlyArgPheValIleGlyGlyProHisGlyAspAlaGlyLeuTh 282
QY 826 CGGCCGCAAGATCATCATCTTACCGAGGATGGGTGCTCATGTTGTTGTTGTTGTTGTT 885
Db 282 rGlyArgLysIleIleIleAspThrTyrGlyGlyTyrPheGlyAlaHisGlyGlyAlaPh 302
QY 886 CTCCGGGAAGGATCCCAACCAAGTTGATAGAGTGGTCTTACATTGTGACACAGGCTGC 945
Db 302 eSerGlyLysAspProThrLysValAspArgSerGlyAlaTyrIleValArgGlnAlaAl 322
QY 946 TAAGCAGATTCTCAACATTGTGAAGAGAACTTTGATTTCAGGCCGCTATGATCTCCAT 1005
Db 322 aLysSerIleValAlaSerGlyLeuAlaArgCysIleValGlnValSerTyrAlaAl 342
QY 1006 TGGTGTGCCCGAGGCTTTGCTCTTTTGTGTGACACCTATGCGACCGGAGAGATCCATGA 1065
Db 342 eGlyValProGluProLeuSerValPheValAspThrTyrGlyThrGlyLysIleHisAs 362
QY 1066 TAAGCAGATTCTCAACATTGTGAAGAGAACTTTGATTTCAGGCCGCTATGATCTCCAT 1125
Db 362 pLysGluLeuLeuAenIleValLysGluAenPheAspPheArgProGlyMetIleSerAl 382
QY 1126 CAACCTTGATCTCAAGAGGGGTGGAAATAACAGGTTCTTGAAGACTGCTGCATATGACA 1185
Db 382 eAsnLeuAspLeuLysArgGlyGlyAsnAsnArgPheLeuLysThrAlaAlaTyrGlyHi 402
QY 1186 CTTGGCAGAGAGGACCCCTGACTTCACATGGGAAGTGGTCAAGCCCTCAAGTGGGAGAA 1245
Db 402 sPheGlyArgGluAspProAspPheThrTrpLysValLysProLeuLysTrpGluLys 422
QY 1246 GGCC 1249
Db 422 sAla 423

RESULT 14
US-10-425-114-71903
; Sequence 71903, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 71903
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700746279_FLI.pbp
US-10-425-114-71903

Alignment Scores:
Pred. No.: 7,3e-193 Length: 423
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Score: 2149.00 Matches: 409  
Percent Similarity: 97.63% Conservativity: 3  
Best Local Similarity: 96.92% Mismatches: 3  
Query Match: 78.20% Indels: 7  
DB: 15 Gaps: 1

US-10-734-698A-38 (1-1485) x US-10-425-114-71903 (1-423)

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QY 4 CAAGCCCCACTCAACACACACACACT-----CTCTCTGCTCTTCTT 45
DB 3 GlnAlaProLeuAenHisHisThrSerProArgSerArgTyrProPhe-LeuLeuPhePh 22
QY 46 CTACCTTTCAAGTTTTTAAAGTATTAAAGATGCGAGACATCTCTATTACCTCAGAGTC 105
DB 22 eTyrLeuSerSerPheLysSerIleLysMetAlaGluThrPheLeuPheThrSerGluSe 42
QY 106 AGTGAACGAGGACACCTCAGACGCTCTCGACCAAAATCTCGATCGCTGCTCTCCAGCG 165
DB 42 rValAsnGluGlyHisProAspLysLeuCyAspGlnIleSerAspAlaValLeuAspAl 62
QY 166 TTGCTTTGAACAGGACCCAGACGAGGTTCCTCGCAACATGCAACCAAGACCAACTT 225
DB 62 aCysLeuGluGlnAspProAspSerLysValAlaCysGluThrCysThrLysThrAsnLe 82
QY 226 GGTATGCTTTCGAGAGATCAACCAAGGCCAACGTTGACTACGAGAAATCGTGG 285
DB 82 uValMetValPheGlyGluIleThrThrLysAlaAsnValAspTyrGluLysIleValAr 102
QY 286 TGACACCTGAGCAACATCGCTCTCAACAGATGCGGACTTGGGACTTGATCTGACAACTG 345
DB 102 gAspThrCysArgAsnIleGlyPheValSerAsnAspValGlyLeuAspAlaAspAsnC 122
QY 346 CAAGGCTCTTGTAAACATTCAGCAGCAGACCCCTGATATTGCCAGCGGTGTCACCGCCA 405
DB 122 sLysValLeuValAsnIleGluGlnSerProAspIleAlaGlnGlyValHisGlyHi 142
QY 406 CTTTACAAAGACCCGAGAAATCGGTGTCGAGACCAAGGTCATCATGTTGGCTATGC 465
DB 142 sLeuThrLysLysProGluGluIleGlyAlaGlyAspGlnGlyHisMetPheGlyTyrAl 162
QY 466 CAGGAGCAACCCAGATTTGATGCTTTCATGATGCTTTCGCACTTAACTCCGCTGC 525
DB 162 aThrAspGluThrProGluLeuMetProLeuSerHisValLeuAlaThrLysLeuGlyAl 182
QY 526 TCCTCTCACCGAGTTTCGAAAGACGAACTCCCATGTTGAGCGCTGATGGGAAAC 585
DB 182 aArgLeuThrGluValArgLysAsnGlyThrCysProThrLeuArgProAspGlyLysTh 202
QY 586 CCAAGTGACTGTTGAGTATTACATCAACACGCTGCCATGGTTCCAGTTTCGTTCCACAC 645
DB 202 rGlnValThrValGluTyrTyrAsnAspAsnGlyAlaArgValProIleArgValHisTh 222
QY 646 TGTGCTTATCTCCACCAACATGATGAGCTGTGACCAAGCAGCAAAATTCAGCTGACCT 705
DB 222 rValLeuIleSerThrGlnHisAspGluThrValThrAsnAspGluIleAlaAlaAspLe 242
QY 706 CAAGGAGCATGTATCAAGCGCTGATCCCGAGAAAGTACCTTGTATGAGAAGACCAATTT 765
DB 242 uLysGluHisValIleLysProValIleProGluLysTyrLeuAspGluLysThrIlePh 262
QY 766 CCACTTGAACCCCTCTGGCGGTTTTGTCAATTGAGAGTCTTCACGGTGATGCTGGTCTCAC 825
DB 262 eHisLeuAsnProSerGlyArgPheValIleGlyGlyProHisGlyAspAlaGlyLeuTh 282
QY 826 CGGCCCCAGATCATCATGATATTACGAGAGATGGGTGCTCATCGTGGTGGTCTTT 885
DB 282 rGlyArgLysIleIleAspThrTyrGlyGlyThrPglyAlaHisGlyGlyGlyAlaPh 302
QY 886 CTCGGGGAAGGATCCCAACCAAGTTGATAGGAGTGTCTTACATTGTGAGACAGGCTGC 945
DB 302 eSerGlyLysAspProThrLysValAspArgSerGlyAlaTyrIleValArgGlnAlaI 322
QY 946 TAAGAGCATTTGTGGCAAGTGGACTAGCCAGAGGTCATTTGTGCAAGTGTCTTATGCCAT 1005
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DB 322 aLysSerIleValAlaSerGlyLeuAlaArgGlyCysIleValGlnValSerTyrAlaI 342
QY 1006 TGTGTGCGCCGAGCCTTCTGCTGCTTTCACACCTATGGCAGCGGAAGATCCATGA 1065
DB 342 eGlyValProGluProLeuSerValPheValAspThrTyrGlyThrGlyLysIleHisAs 362
QY 1066 TAAGGAGATTCTCAACATTGTGAAGGAGAACTTTGATTTTCAGCCCGGTATGATCTCCAT 1125
DB 362 pLysGluIleLeuAenIleValLysGluAsnPheAspPheArgProGlyMetIleSerIl 382
QY 1126 CAACCTTGATCTCAAGAGGGTGGGAATAACAGGTTCTTGAAGACTGCTGCATATCGACA 1185
DB 382 eAsnLeuAspLeuLysArgGlyGlyAsnAsnArgPheLeuLysThrAlaAlaTyrGlyHi 402
QY 1186 CTTGCGCAGAGGACCCCTGACTTCACATGCGGAAGTGGTCAAGCCCTCCAAGTGGGAGAA 1245
DB 402 sPheGlyArgGluAspProAspPheThrTrpGluValValLysProLeuLysTrpGluLy 422
QY 1246 GCCC 1249
DB 422 sAla 423
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## RESULT 15

US-10-425-114-71916  
; Sequence 71916, Application US/10425114  
; Publication No. US2004003488A1

## GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(5313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 71916  
; LENGTH: 423  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700747550\_FLI.pap  
US-10-425-114-71916

## Alignment Scores:

Pred. No.: 7,3e-193 Length: 423  
Score: 2149.00 Matches: 409  
Percent Similarity: 97.63% Conservativity: 3  
Best Local Similarity: 96.92% Mismatches: 3  
Query Match: 78.20% Indels: 7  
DB: 15 Gaps: 1

US-10-734-698A-38 (1-1485) x US-10-425-114-71916 (1-423)

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QY 4 CAAGCCCCACTCAACACACACACACT-----CTCTCTGCTCTTCTT 45
DB 3 GlnAlaProLeuAenHisHisThrSerProArgSerArgTyrProPhe-LeuLeuPhePh 22
QY 46 CTACCTTTCAAGTTTTTAAAGTATTAAAGATGCGAGACATCTCTATTACCTCAGAGTC 105
DB 22 eTyrLeuSerSerPheLysSerIleLysMetAlaGluThrPheLeuPheThrSerGluSe 42
QY 106 AGTGAACGAGGACACCTCAGACGCTCTCGCAACAAATCTCCGATGCTGTCTCGACGC 165
DB 42 rValAsnGluGlyHisProAspLysLeuCyAspGlnIleSerAspAlaValLeuAspAl 62
QY 166 TTGCTTTGAACAGGACCCAGACGAGGTTCCTCGGNAACATGCAACCAAGACCAACTT 225
DB 62 aCysLeuGluGlnAspProAspSerLysValAlaCysGluThrCysThrLysThrAsnLe 82
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Search completed: August 25, 2005, 17:35:57  
Job time : 249 secs

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QY 226 GGTCTGCTCTTCGGAGAGATCACCAAGCCAAAGCTTGACTAGGAGAAGATCGTGG 285
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QY 82 uValMetValPheGlyGluIleThrThrLysAlaAsnValAsePThrGlyLysIleValAr 102
Db |||||||
QY 286 TGACACCTGCAGGAACATCGGCTTCGCTCTCAACCATGTGGGACTTGATCTGACAACATG 345
Db |||||||
QY 102 gAspThrCysArgAsnIleGlyPheValSerAsnAspValGlyLeuAspAlaAspAsnCy 122
Db |||||||
QY 346 CAAAGTCTCTTGAACATTGAGCAGCAGCCCTGATATTGCCAGGGGTGTCACGGCCA 405
Db |||||||
QY 122 sLysValLeuValAsnIleGluGlnSerProAspIleAlaGlnGlyValHisGlyHi 142
Db |||||||
QY 406 CTTTACCAAAAGACCCGAGGAATCGGTCTCGAGACACGAGGTCCATGTTTGGCTATGC 465
Db |||||||
QY 142 sleuthrLysLysProGluGluIleGlyAlaGlyAspGlnGlyHisMetPheGlyTyAl 162
Db |||||||
QY 466 CACGACGAACCCAGAAATGATGCCATTGATGCTCATGTTCTTGCAACTTAAACTCGGTGC 525
Db |||||||
QY 162 aThrAspGluThrProGluLeuMetProLeuSerHisValLeuAlaThrLysLeuGlyAl 182
Db |||||||
QY 526 TGGTCTCACCGAGTTCCGAAGAACCGAACCTGCCCATGGTTGAGGCCCTGATGGGAAAAC 585
Db |||||||
QY 182 aArgLeuThrGluValArgLysAsnGlyThrCysProTrpLeuArgProAspGlyLysTh 202
Db |||||||
QY 586 CCAAGTGACTGTTGAGTATTCAATGACAAACGGTGCATGTTCCAGTTCGTGTCCACAC 645
Db |||||||
QY 202 rGlnValThrValGluTyTyAsnAspAsnGlyAlaArgValProIleArgValHisTh 222
Db |||||||
QY 646 TGTGCTTATCTCCACCAACATGATGAGACTGTGACCAACGACGAAATTCAGCTGACCT 705
Db |||||||
QY 222 rValLeuIleSerThrGlnHisAspGluThrValThrAsnAspGluIleAlaAspLe 242
Db |||||||
QY 706 CAAAGAGCATGTGATCAACCGGTGATCCCGAGAGTACCTTGATGAGAACCATTTT 765
Db |||||||
QY 242 uLysGluHisValIleLysProValIleProGluLysTyLeuAspGluLysThrIlePh 262
Db |||||||
QY 766 CCACCTTGAACCTCTCGGCCGTTTGTCTATTGGAGTCTCTCACGGTGTGCTGCTCAC 825
Db |||||||
QY 262 eHisLeuAenProSerGlyArgPheValIleGlyGlyProHisGlyAspAlaGlyLeuth 282
Db |||||||
QY 826 CGGCCCAAGATCATCATGACTTACGAGAGTGGGTGCTCATGTTGGTGGTCTTT 885
Db |||||||
QY 282 rGlyArgLysIleIleIleAspThrTyrglyGlyTyrglyAlaHisGlyGlyValaPh 302
Db |||||||
QY 886 CTCCGGGAAGGATCCCAAGGTTGATAGAGTGGTCTTACATTGTGAGACAGGCTGC 945
Db |||||||
QY 302 eSerGlyLysAspProThrLysValAspArgSerGlyAlaTyriIleValArgGlnAlaAl 322
Db |||||||
QY 946 TAAGAGCATTTGGCAAGTGGACTAGCCAGAGGTGCATTGTGCAAGTGTCTTATGCCAT 1005
Db |||||||
QY 322 aLysSerIleValAlaSerGlyLeuAlaArgCysIleValGlnValSerTyAlaAl 342
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QY 1006 TGTGTGCCCGAGCTTCTGCTCTTCTGCTTGTGACACTATGGCACCGGGAAGATCCATGA 1065
Db |||||||
QY 342 eGlyValProGluProLeuSerValPheValAspThrTyrglyThrGlyLysIleHisAs 362
Db |||||||
QY 1066 TAAGGAGATTCTCAACATTGTGAAGGAGAACTTTGATTTACGGCCGGTATGATCTCCAT 1125
Db |||||||
QY 362 pLysGluIleLeuAsnIleValLysGluAsnPheAspPheArgProGlyMetIleSerIl 382
Db |||||||
QY 1126 CAACCTTGATCTCAGAGGGTGGGAATAACAGGTTCTTGAAGACTGCTGCATATGGACA 1185
Db |||||||
QY 382 eAsnLeuAspLeuLysArgGlyGlyAsnAsnArgPheLeuLysThrAlaIaIaTyrglyHi 402
Db |||||||
QY 1186 CTTCCGCACAGAGGACCTGACTTCATGCGGAAGTGGTCAAGCCCTCAAGTGGGAGAA 1245
Db |||||||
QY 402 sPheGlyArgGluAspProAspPheThrTrpGluValValLysProLeuLysTrpGluLy 422
Db |||||||
QY 1246 GGCC 1249
Db |||||
QY 422 sAla 423
Db |||||
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GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: August 25, 2005, 17:03:11 ; Search time 60 Seconds  
(without alignments)  
4762.730 Million cell updates/sec

Title: US-10-734-698A-38  
Perfect score: 2748  
Sequence: 1 ACCCAAGCCCCCTCAACCA.....CAAAGAATGTTCCAAAGTT 1485

Scoring table:

BLOSUM62	
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566932

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ n2p.model -DEV=xlp  
-O=/cn2\_1/usPTO\_spool\_p/us10734698/runat\_25082005\_105401\_10285/app\_query.fasta\_1.1671  
-DB=PIR -QPMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -LIST=45  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10734698 @CN 1 1.80 @runat\_25082005\_105401\_10285 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -XGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR.79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1985	72.2	393	2	S46538 methionine adenosy
2	1983	72.2	393	2	S38875 methionine adenosy
3	1947	70.9	393	2	JQ0410 methionine adenosy
4	1940	70.6	393	2	C86155 S-adenosylmethioni
5	1937	70.5	393	2	JN0131 methionine adenosy
6	1932.5	70.3	396	2	T10710 methionine adenosy
7	1920.5	69.9	397	2	S68352 methionine adenosy
8	1900.5	69.2	394	2	T06180 methionine adenosy
9	1884	68.6	390	2	S46540 methionine adenosy
10	1872	68.1	390	2	G84785 probable s-adenosy
11	1857	67.6	390	2	S49491 methionine adenosy
12	1803	65.6	366	2	S66351 methionine adenosy
13	1742	63.4	360	2	T06592 methionine adenosy
14	1316.5	47.9	395	1	S27257 methionine adenosy

ALIGNMENTS

RESULT 1

S46538  
methionine adenosyltransferase (BC 2.5.1.6) - tomato  
N/Alternate names: S-adenosyl-L-methionine synthetase  
C/Species: Lycopersicon esculentum (tomato)  
C/Date: 26-Dec-1994 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
C/Accession: S46538; S38874  
R/Submitter: J. Pintor-Toro, J.A.; Pardo, J.M.  
A/Title: Differential accumulation of S-adenosylmethionine synthetase transcripts in res.  
Plant Mol. Biol. 25, 217-227, 1994  
A/Reference number: S46538; MUID:94289646; PMID:8018871  
A/Accession: S46538  
A/Status: nucleic acid sequence not shown  
A/Molecule type: mRNA  
A/Residues: 1-393 <ESP>  
A/Cross-references: UNIPROT:P43280; EMBL:Z24741; NID:G429103; PIDN:CAA80865.1; PID:G4291  
C/Superfamily: methionine adenosyltransferase  
C/Keywords: S-adenosylmethionine; transferase

Alignment Scores:  
Pred. No.: 8.54e-151 Length: 393  
Score: 1985.00 Matches: 374  
Percent Similarity: 97.69% Conservative: 6  
Best Local Similarity: 96.14% Mismatches: 9  
Query Match: 72.23% Indels: 0  
DB: 2 Gaps: 0  
US-10-734-698A-38 (1-1485) x S46538 (1-393)  
QY 80 GAGACATTCCTATTACCTGAGTCACTGAACGAGGACACCTTGACAGCTCTCGGAC 139  
DB 2 GlutThrPheLeuPheThrSerGluSerValaenGluGlyHisProAspIysLeuCysasp 21  
QY 140 CAATCTCCGATGCTGCTCCTCGACCTTGCTTGAACAGGACCCAGACAGCAGGTTGCC 199  
DB 22 GlnIleSerAspAlaValLeuAspIaCysLeuGluInaAppProGluSerIysValaIa 41  
QY 200 TCGGAACATGCACCAAGACCACTTGTGTCATGTTTCGAGAGATCACCACCAAGGCC 259

15 1310.5 47.7 395 2 A37118 methionine adenosy  
16 1274.5 46.4 382 2 T39451 methionine adenosy  
17 1268.5 46.2 396 2 A47151 methionine adenosy  
18 1268 46.1 397 2 S06114 methionine adenosy  
19 1264 46.0 395 2 S65800 methionine adenosy  
20 1262.5 45.9 395 1 S27363 methionine adenosy  
21 1209.5 44.0 404 2 T34085 hypothetical prote  
22 1209.5 44.0 404 2 T34084 hypothetical prote  
23 1205 43.9 419 2 T16856 methionine adenosy  
24 1198.5 43.6 382 2 S51425 methionine adenosy  
25 1198 43.6 403 2 T20070 hypothetical prote  
26 1191.5 43.4 384 2 A31398 methionine adenosy  
27 1180 42.9 359 2 T47208 methionine adenosy  
28 1167.5 42.5 399 2 D84062 S-adenosylmethioni  
29 1156.5 42.1 405 2 S41917 methionine adenosy  
30 1137 41.4 395 2 G72228 S-adenosylmethioni  
31 1114 40.5 400 2 D69657 methionine adenosy  
32 1106.5 40.3 391 2 D97251 S-adenosylmethioni  
33 1104 40.2 399 2 AD1654 S-methionine adeno  
34 1100.5 40.0 389 2 D81042 S-adenosylmethioni  
35 1096.5 39.9 398 2 F89964 probable methionin  
36 1093.5 39.8 389 2 E81986 S-methionine adeno  
37 1091 39.7 399 2 AH1282 hypothetical prote  
38 1072 39.0 363 2 T26385 S-adenosylmethioni  
39 1069.5 38.9 384 2 AB0877 methionine adenosy  
40 1068.5 38.9 384 1 SYECSM methionine adenosy  
41 1068.5 38.9 384 2 B91106 methionine adenosy  
42 1068.5 38.9 384 2 E85951 methionine adenosy  
43 1062.5 38.7 396 2 G97955 methionine adenosy  
44 1060 38.6 385 2 E82319 S-adenosylmethioni  
45 1058 38.5 388 2 S51671 methionine adenosy

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42 CysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluLeuThrThrLysAla 61  
260 AAGTTGACTACGAGAAATCGTGGTGTACCTGCGAGAAACATCGGCTTCGTCTCAAAC 319  
Db |||||  
62 lIeValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheValSerAsp 81  
Qy |||||  
320 GATGTGGACTTGATGCTGACAACTGCAAGTCCCTTGTAAACATTTGAGCAGCAGACCGCT 379  
Db |||||  
82 AspValGlyLeuAspAlaAspAsnCysLysValLeuValTyrIleGluGlnSerPro 101  
Qy |||||  
380 GATATTGCCAGGGTGTGCACGCCACCTTACCAAAAGACCCGAGGAAATCGGTCTGGA 439  
Db |||||  
102 AspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGlyAlaGly 121  
Qy 440 GACACGGGTACATGTTGGCTATGCCACGGAAGAAACCCCAAGAAATTTGATGATGAGT 499  
Db |||||  
122 AspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuSer 141  
Qy |||||  
500 CATGTTCTTCAACTAACTCGTCTGCTCACCGAGTTCGCAAGAACCGACCTGTC 559  
Db |||||  
142 HisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThrCys 161  
Qy 560 CCATGTTGAGCGCTGATCGGGAACCCCAAGTCACTGTTGAGTATTACAATGACACCGT 619  
Db |||||  
162 AlaTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrSerAsnAspGly 181  
Qy 620 GCATGTTCCAGTTCGTGTCACACTGTGCTTATCTCCACCAACATGATGAGTGTG 679  
Db |||||  
182 AlaMetValProIleArgValHisThrValLeuIleSerThrGlnHisAspGluThrVal 201  
Qy 680 ACCACGAGAAATTCACCTGACCTCAAGGAGCATGTGATCAAGCCGTGATCCGGAG 739  
Db |||||  
202 ThrAsnAspGluIleAlaArgAspLeuLysGluHisValIleLysProValIleProGlu 221  
Qy 740 AAGTACTTGTGAGAGAACCACTTTTCCACTTTGAAACCCCTCTCGGCCGTTTGTCTATTGGA 799  
Db |||||  
222 LysTyrLeuAspGluAsnThrIlePheHisLeuAsnProSerGlyArgPheValIleGly 241  
Qy 800 GTCTCTACGGTGATGCTGGTCTCACCGGCCGCAAGATCATCATGACTTACCGAGA 859  
Db |||||  
242 GlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyrGlyGly 261  
Qy 860 TGGGTGTCTCATGGTGGTGTCTTCCCGGAAGGATCCCAACAGGTGATAGGAGT 919  
Db |||||  
262 TrpGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSer 281  
Qy 920 GGTGTTTACATTGTGAGACAGCTGTCTAAGAGCATTTGTGGCAAGTGGACTAGCCAGAAGG 979  
Db |||||  
282 GlyAlaTyrIleValArgGlnAlaLysSerIleValAlaSerGlyLeuAlaArgArg 301  
Qy 980 TGCATTGTCCAGTGTCTTATGCCATTGTGTGTCGGAGCCCTTGTCTGCTTTGTGAC 1039  
Db |||||  
302 CysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAsp 321  
Qy 1040 ACCTATGGCAGCGGAGATCCATGATAGGAGATCTCAACATTTGTGAAGGAGACTTT 1099  
Db |||||  
322 ThrTyrGlyThrGlyLysIleProAspArgGluIleLeuLysIleValLysGluAsnPhe 341  
Qy 1100 GATTTCCAGCCGGTATGATCTCCATCAACCTTGTATCTCAAGAGGGGTGGGAATAACAGG 1159  
Db |||||  
342 AspPheArgProGlyMetMetSerIleAsnLeuAspLeuLysArgGlyGlyAsnArgArg 361  
Qy 1160 TTCTTGAAGACTGCTGCATATGACATTCCTCGGAGAGGACCTGACTTCAATGAGGAA 1219  
Db |||||  
362 PheLeuLysThrAlaAlaTyrGlyHisPheGlyArgAspAspProAspPheThrTrpGlu 381  
Qy 1220 GTGGTCAAGCCCTCAAGTGGGAGAG 1246  
Db |||||  
382 ValValLysProLeuLysTrpGluLys 390

methionine adenosyltransferase (EC 2.5.1.6) - tomato  
N:Alternate names: S-adenosyl-L-methionine synthetase  
C:Species: Lycopersicon esculentum (tomato)  
C:Date: 22-Jan-1994 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
C:Accession: S46539; S38875  
R:Espartero, J.; Pintor-Toro, J.A.; Pardo, J.M.  
Plant Mol. Biol. 25, 217-227, 1994  
A:Title: Differential accumulation of S-adenosylmethionine synthetase transcripts in res  
A:Reference number: S46538; MUID:94289646; PMID:8018871  
A:Accession: S46539  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-393 <ES2>  
A:Cross-references: UNIPROT:P43281; EMBL:Z24742; NID:9429105; PIDN:CAA80866.1; PID:9429105  
C:Superfamily: methionine adenosyltransferase  
C:Keywords: S-adenosylmethionine; transferase

Alignment Scores:  
Pred. No.: 1,24e-150 Length: 393  
Score: 1983.00 Matches: 371  
Percent Similarity: 97.69% Conservative: 9  
Best Local Similarity: 95.37% Mismatches: 9  
Query Match: 72.16% Indels: 0  
DB: 2 Gaps: 0

US-10-734-698A-38 (1-1485) x S38875 (1-393)

Qy 80 GAGACATTCCTATTACCTCAGAGTCAGTGAACGAGGGACACCTTGACAAAGCTCTGGCAC 139  
Db 2 GluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCysAsp 21  
Qy 140 CAATCTCCGATGCTGCTCGAGCTTGCCTTGAACAGGACCCAGACAGCAAGGTTGCC 199  
Db |||||  
22 GlnValSerAspAlaValLeuAspAlaCysLeuAlaGlnAspProGluLysValAla 41  
Qy 200 TCGGAAAACATGCACCAAGACCAACCTTGTGTCATGCTTTCGAGAGATCACCACCAAGGCC 259  
Db |||||  
42 CysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluLeuThrThrLysAla 61  
Qy 260 AAGTTGACTACGAGAAATCGTGGTGTACACCTGCGAGAAACATCGGCTTCGTCTCAAC 319  
Db |||||  
62 AsnIleAspTyrGluLysIleValArgAspThrCysArgGluIleGlyPheValSerPro 81  
Qy 320 GATGTGGACTTGATGCTGACAACTGCAAGTTCCTTGTAAACATTTGAGCAGCAGACCGCT 379  
Db |||||  
82 AspValGlyLeuAspAlaAspAsnCysArgValLeuValAsnIleGluGlnSerPro 101  
Qy 380 GATATTGCCAGGGTGTGCACGCCACCTTACCAAAAGACCCGAGGAAATCGGTCTGGA 439  
Db |||||  
102 AspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGlyAlaGly 121  
Qy 440 GACACGGGTACATGTTGGCTATGCCACGAGCAAGAACCCCAAGAAATTTGATGAGTGTG 499  
Db |||||  
122 AspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuSer 141  
Qy 500 CATGTTCTTCAACTAACTCGTCTGCTCACCGAGGTTTCGCAAGAACCGACCTGTC 559  
Db |||||  
142 HisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThrCys 161  
Qy 560 CCATGTTGAGCGCTGATCGGGAACCCCAAGTCACTGTTGAGTATTACAATGACACCGT 619  
Db |||||  
162 SerTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrHisAsnAspGly 181  
Qy 620 GCATGTTCCAGTTCGTGTCACACTGTGCTTATCTCCACCAACATGATGAGACTGTG 679  
Db |||||  
182 AlaMetValProLeuArgValHisThrValLeuIleSerThrGlnHisAspGluThrVal 201  
Qy 680 ACCACGAGAAATTCACCTGACCTCAAGGAGCATGTGATCAAGCCGTGATCCCGAG 739  
Db |||||  
202 ThrAsnAspGluIleAlaArgAspLeuLysGluHisValIleLysProValIleProGlu 221  
Qy 740 AAGTACCTTGTGAGAGAACCACTTTCCACTTTGAAACCCCTCTCGGCCGTTTGTCTATTGGA 799  
Db |||||

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Db      222 LysTyrLeuAspGluAsnThrIlePheHisLeuAsnProSerGlyArgPheValIleGly 241
QY      800 GGTCTCTCAGCGTATGCTGTCTCACCGCGCGCAAGATCATATCATGATATTACGAGGA 859
Db      242 GlyProHisGlyAspIleGlyLeuThrGlyArgLysIleIleIleAspThrTyrGlyGly 261
QY      860 TGGGGTGCTCATGGTGGTGGTCTTCTCCGGGAAGGATCCCAACCAAGTTGATAGGAGT 919
Db      262 TrpGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSer 281
QY      920 GTGTCTTACATTGTGAGACAGCTGTAAAGCATTTGTGGCAAGTGGACTAGCCAGAGG 979
Db      282 GlyAlaTyrIleValArgGlnAlaAlaLysSerIleValAlaAsnIleValAlaArgArg 301
QY      980 TGCAATGTGCAAGTGTCTTATGTCATTGGTGTGCGCGCGCTTGTCTGTCTTTGTGAC 1039
Db      302 CysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAsp 321
QY      1040 ACTATGTGCACCGGGAAGATCCATATAAGGAGATTCTCAACATTGTGAAGGAACTTTT 1099
Db      322 ThrTyrGlyThrGlyLysIleProAspLysGluIleLeuAsnIleValLysGluAsnPhe 341
QY      1100 GATTTCAGCGCCGGTATGATCTCAACCTTGATCTCAAGAGGGGTGGGAATACAGG 1159
Db      342 AspPheArgProGlyMetIleSerIleAsnLeuAspLeuLeuArgGlyAsnGlyArg 361
QY      1160 TTCTTGAAGACTGCTCATATGACACTTCGGCAGAGAGCACCTGACTTCAATGGGAA 1219
Db      362 PheLeuLysThrAlaAlaTyrGlyHisPheGlyArgAspAspPheThrTrpGlu 381
QY      1220 GTGGTCAAGCCCTCAAGTGGGAGAG 1246
Db      382 ValValLysProLeuLysTrpAspLys 390

RESULT 3
JQ0410
methionine adenosyltransferase (EC 2.5.1.6) 2 - Arabidopsis thaliana
N:Alternate names: S-adenosylmethionine synthetase
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C:Accession: JQ0410
R:Peleman, J.; Saijo, K.; Cottyn, B.; Engler, G.; Seurinck, J.; Van Montagu, M.; Inze, D
Gene 84, 359-369, 1989
A:Title: Structure and expression analyses of the S-adenosylmethionine synthetase gene f
A:Reference number: JQ0410, MUID:90128280; PMID:2482229
A:Accession: JQ0410
A:Molecule type: DNA
A:Residues: 1-393 <PEL>
A:Cross-references: UNIPROT:P17562; GB:M33217; NID:g166873; PIDN:AAA32869.1; PID:g166874
C:Genetics:
C:Superfamily: methionine adenosyltransferase
C:Keywords: S-adenosylmethionine; transferase

Alignment Scores:
Pred. NO.:          9,46e-148      Length:          393
Score:             1947.00         Matches:         360
Percent Similarity: 96.92%         Conservatives:    17
Best Local Similarity: 92.54%      Mismatches:      12
Query Match:       70.85%          Indels:          0
DB:                2              Gaps:            0

US-10-734-698A-38 (1-1485) x JQ0410 (1-393)

QY      80 GAGACATTCCTATTACCTCAGAGTCAGTGAACGAGGGAACCCCTGACAGCTCTCGGAC 139
Db      2 GluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCysAsp 21
QY      140 CAAATCTCCGATGCTGCTCTCCAGCGCTTCTTGAACAGAGCCCGAGACAGGAGTGGCC 199
Db      22 GlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLysValAla 41
QY      200 TGCAGAAACATGCACCAAGACCAACTTGGTTCATGGTCTTCGGAGAGATCACCAAGGCC 259
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RESULT 4  
C86155

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Db      42 CysGluThrCysThrLysThrAsnMetValMetValPheGlyGluIleThrThrLysAla 61
QY      260 AACGTTGACTACGAGAAGATCGTGGTGCACCTCGCAGCAACATCGGCTTCTCTCTCAAC 319
Db      62 ThrIleAspTyrGluLysIleValArgAspThrCysArgSerIleGlyPheIleSerAsp 81
QY      320 GATGTGGACATTTGATGTCACAACATGCAAGGTCTTGTAAACATTGAGCAGAGACCCCT 379
Db      82 AspValGlyLeuAspAlaAspLysCysLysValLeuValAsnIleGluGlnGlnSerPro 101
QY      380 GATATTGCCAGGGTGTGCACGGCCACCTTACCAGAAACCCGAGAGAAATCGGTGCTGA 439
Db      102 AspIleAlaGlnGlyValHisGlyHisPheThrLysArgProGluAspIleGlyAlaGly 121
QY      440 GACCAAGGTGCATGCTTTGGCTATGCCACGAGCAAAACCCCAAGATTGATGCCATTGAGT 499
Db      122 AspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuSer 141
QY      500 CATGTTCTTCAACATAACTCGGTGCTGCTCTCACGAGGTTTCGCAAGAACGAACTGTC 559
Db      142 HisValLeuAlaThrLysIleGlyAlaArgLeuThrGluValArgLysAsnGlyThrCys 161
QY      560 CCATGTTGAGGCTGATGGGAAAACCCCAAGTACTGTTGAGTATATACATGACAAACGGT 619
Db      162 ArgTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnAspAsnGly 181
QY      620 GCCATGTTTCAGATTTCGTTCCACACTGCTTATCTCCACCAACATGATGAGACTGTG 679
Db      182 AlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGluThrVal 201
QY      680 ACCAACGACGAAATTCAGCTGACCTCAAGGAGCATGTGATCAAGCCGGTGTATCCGGAG 739
Db      202 ThrAsnAspGluIleAlaArgAspLeuLysGluHisValIleLysProIleIleProGlu 221
QY      740 AAGTACTTGTATGAGAGAACCATTTTCCATTGTAACCCCTCTGCGCGTTTGTCTATTGA 799
Db      222 LysTyrLeuAspAspLysThrIlePheHisLeuAsnProSerGlyArgPheValIleGly 241
QY      800 GGTCTCAGCGTGTGCTGTCTCACCGCGCGCAAGATCATCATCGTACTTACCGAGGA 859
Db      242 GlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleIleAspThrTyrGlyGly 261
QY      860 TGGGGTGCTCATGGTGGTGGTCTTCTCCGGGAAGGATCCCAACCAAGTTGATAGGAGT 919
Db      262 TrpGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSer 281
QY      920 GGTCTTACATTGTGAGACAGCTGTAAAGCATTTGTGGCAAGTGGACTAGCCAGAGG 979
Db      282 GlyAlaTyrIleValArgGlnAlaAlaLysSerValValAlaAsnGlyMetAlaArgArg 301
QY      980 TGCATTGTGCAAGTGTCTTATGTCATTGGTGTGCGCGCGCTTGTCTGTCTTCTTGTGAC 1039
Db      302 AlaLeuValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAsp 321
QY      1040 ACCTATGTCACCGGGAAGATCCATGATAAGGAGATTCTCAACATTGTGAAGGAGAACTTT 1099
Db      322 ThrTyrGlyThrGlyLeuIleProAspLysGluIleLeuLysIleValLysGluThrPhe 341
QY      1100 GATTTCAGCGCCGGTATGATCTCAACCTTGATCTCAAGAGGGGTGGGAATACAGG 1159
Db      342 AspPheArgProGlyMetMetThrIleAsnLeuAspLeuLysArgGlyGlyAsnGlyArg 361
QY      1160 TTCTTGAAGACTGCTCATATGACACTTCGGCAGAGAGCACCTGACTTCAATGGGAA 1219
Db      362 PheGlnLysThrAlaAlaTyrGlyHisPheGlyArgAspAspPheThrTrpGlu 381
QY      1220 GTGGTCAAGCCCTCAAGTGGGAGAG 1246
Db      382 ValValLysProLeuLysTrpAspLys 390
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S-adenosylmethionine synthetase [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: C86155  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; aneen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.-C.A.; Li, J.H.; Lin, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: C86155  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-393 <STO>  
A:Cross-references: UNIPROT:P23686; GB:AE005172; NID:g9972389; PIDN:AAG10639.1; GSPDB:GN  
C:Genetics:  
C:Superfamily: methionine adenosyltransferase  
A:Map position: 1  
C:Superfamily: methionine adenosyltransferase

Alignment Scores:  
Pred. No.: 3,44e-147 Length: 393  
Score: 1940.00 Matches: 363  
Percent Similarity: 96.40% Conservative: 12  
Best Local Similarity: 93.32% Mismatches: 14  
Query Match: 70.60% Indels: 0  
DB: 2 Gaps: 0

US-10-734-698a-38 (1-1485) x C86155 (1-393)

QY 80 GAGACATTCCTATTTACCTCAGAGTCAGTGAACGAGGGACACCTGACAAAGCTCTGCGAC 139  
Db 2 GluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCysAsp 21  
QY 140 CAATCTCCGATGCTGCTCGACGCTTCCTTGACAGGACCCAGACGAGAGGTGCC 199  
Db 22 GlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLysValAla 41  
QY 200 TCGCAACATGACCAAGACCACTTGGTCATGGTCTTCGGAGAGATCACCAACGAGGCC 259  
Db 42 CysGluThrCysThrLysThrAsnMetValMetValPheGlyGluIleThrThrLysAla 61  
QY 260 AACGTTGACTACGAGAAGATCGTGGCTGACACCTCGAGAAACATCGGCTTCGTCAAC 319  
Db 62 ThrValAspTyrGluLysIleValArgAspThrCysArgAlaIleGlyPheValSerAsp 81  
QY 320 GATGTGGGACTTGATGCTGACAACTGCAAGGTCTCTGTTAAACATTTGACGACGAGCCCT 379  
Db 82 AspValGlyLeuAspAlaAspLysCysLysValLeuValAsnIleGluGlnSerPro 101  
QY 380 GATATTGCCAGGTGTGACGCGCCACCTTACCAAAAGACCCGAGGAATCGTGCTGA 439  
Db 102 AspIleAlaGlnGlyValHisGlyHisPheThrLysCysProGluGluIleGlyAlaGly 121  
QY 440 GACCGGGTCACATGTTGGCTATGCGACGAGCAACCCCAAGATTGATGCGATTGAGT 499  
Db 122 AspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuSer 141  
QY 500 CATGTTCTTGCACTAACTCGGTGCTGCTCACCAGGTTCGCAAGACCGAACCTGCG 559  
Db 142 HisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThrCys 161  
QY 560 CCATGGTTGAGCGCTGATGGGAAACCCCAAGTGACTGTTGAGTATTACAATCACACCGT 619  
Db 162 AlaTrpLeuArgProAspGlyThrGlnValThrValGluTyrTrpAsnAspLysGly 181  
QY 620 GCCATGGTTCCAGTTCGTCGCACACTGTGCTTATCTCCACCAACATGATGAGACTGTG 679  
Db 182 AlaMetValProIleArgValHisThrValLeuIleSerThrGlnHisAspGluThrVal 201

QY 680 ACCAACGACGAAATTGCAGCTGACCTCAAGSAGCATGTGATCAAGCCGGTGCATCCCGGAG 739  
Db 202 ThrAsnAspGluIleAlaAargAspLeuLysGluHisValIleLysProValIleProGlu 221  
QY 740 AAGTACCTTGATGAGAAGACCATTTTCACATTGAACCCCTCTGGCCGGTTTTGTTCATTGGA 799  
Db 222 LysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheValIleGly 241  
QY 800 GGTCTCAGCGTGATGCTGCTCACCAGCGCGAAGATCATCATCGATCATCTTACGGAGGA 859  
Db 242 GlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyrGlyGly 261  
QY 860 TGGGGTCTCATGCTGTGGTGGCTTCTCCGGGAAGGATCCACCAAGGTTGATAGGAGT 919  
Db 262 TrpGlyAlaHisGlyGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSer 281  
QY 920 GGTGCTTACATTGTGACAGCGCTGCTAAGACGATTTGTGGCAAGTGGACTAGCCAGAGG 979  
Db 282 GlyAlaTyrIleValArgGlnAlaAlaLysSerValValAlaAsnGlyMetAlaArgArg 301  
QY 980 TGCATTTGCAAGTGTCTTATGCCATTGCTGTGCTGCCGAGCCCTTGTCTGTCTTGTTCAC 1039  
Db 302 AlaLeuValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAsp 321  
QY 1040 ACCTATGCGACCGGGAAGATCCATGAAGAGATTTCTCAACATTTGTGAAGAGAACTTT 1099  
Db 322 ThrTyrGluThrGlyLeuIleProAspLysGluIleLeuLysIleValLysGluSerPhe 341  
QY 1100 GATTTCAAGCCCGGTATGATCTCCATCAACCTTGATCTCAAGAGGGGTGGGAATAACAGG 1159  
Db 342 AspPheArgProGlyMetMetThrIleAsnLeuAspLeuLysArgGlyAsnGlyArg 361  
QY 1160 TTCTTGAAGACTGCTGATATGGACACTTCGGCAGAGAGGACCTTGACTTCACATGGGAA 1219  
Db 362 PheLeuLysThrAlaAlaTyrGlyHisPheGlyArgAspProAspPheThrTrpGlu 381  
QY 1220 GTGCTCAAGCCCTCAAGTGGGAGAAG 1246  
Db 382 ValValLysProLeuLysTrpAspLys 390

RESULT 5  
JN0131  
methionine adenosyltransferase (EC 2.5.1.6) - Arabidopsis thaliana  
N:Alternate names: S-adenosylmethionine synthetase  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 09-Jul-2004  
C:Accession: JN0131  
R:Peleman, J.; Boerjan, W.; Engler, G.; Seurinck, J.; Botterman, J.; Alliotte, T.; Van N  
Plant Cell 1, 81-93, 1989  
A:Title: Strong cellular preference in the expression of a housekeeping gene of Arabidop  
A:Reference number: JN0131; MUID:92386056; PMID:2535470  
A:Accession: JN0131  
A:Molecule type: DNA  
A:Residues: 1-393 <PEL>  
A:Cross-references: UNIPROT:P23686; GB:M55077; NID:g166871; PIDN:AAA32868.1; PID:g166872  
A:Experimental source: var. X85  
A:Note: the sequence derived from var. Columbia differs from that shown in having 117-G  
C:Comment: S-Adenosylmethionine synthetase catalyzes the biosynthesis of adenosylmethio  
A:Gene: sam-1  
A:Superfamily: methionine adenosyltransferase  
C:Keywords: S-adenosylmethionine; transferase

Alignment Scores:  
Pred. No.: 5.99e-147 Length: 393  
Score: 1937.00 Matches: 362  
Percent Similarity: 96.40% Conservative: 13  
Best Local Similarity: 93.06% Mismatches: 14  
Query Match: 70.49% Indels: 0  
DB: 2 Gaps: 0

US-10-734-698A-38 (1-1485) x JN0131 (1-393)

QY 80 GAGACATTCCTATTACCTCAGAGTCAAGAGGAGCACCTCAGACAGCTCTCGAC 139  
Db 2 GluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCysAsp 21  
QY 140 CAAATCTCCGATGCTGCTCGAGCGCTTGCTTGAACAGGACCCAGACAGCAAGTGGC 199  
Db 22 GlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLysValAla 41  
QY 200 TGGAAACATGACCAAGACCACTTGCTCATCGTCTTCGGAGAGATCAACCAAGGCC 259  
Db 42 CysGluThrCysThrLysThrAsnMetValMetValPheGlyGluLeuThrLysAla 61  
QY 260 AAGCTTGACTACGAGAAGATCGTGCCTGACACCTGCAGGAACATCGGCTCTCAAC 319  
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QY 380 GATATTGCCAGGGTGTGCAGCGCCACCTTACCAAAAGACCCGAGGAATCGGTCTGA 439  
Db 102 AspIleAlaGlnGlyValHisGlyHisPheThrLysCysProGluAspIleGlyAlaGly 121  
QY 440 GACAGGGTCACATGTTGGCTATGCCACGAGCAAAACCCAGAAATTTGATGCTTGA 499  
Db 122 AspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuSer 141  
QY 500 CATGTTCTTGCAACTAACTCGGTGCTCTCACCAGAGTTGCGAAGAACGGAACCTGC 559  
Db 142 HisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThrCys 161  
QY 560 CCATGTTGAGGCTCATGCGAAACCCCAAGTCACTGTTGAGTATTACATCAACGCT 619  
Db 162 AlaThrPheLeuArgProAspGlyLysThrGlnValThrValGluTyrTrpAsnAspLysGly 181  
QY 620 GCATGTTCCAGTTCGTGTCACACTGTGCTTATCTCCACCAACATCATGAGACTGTG 679  
Db 182 AlaMetValProIleArgValHisThrValLeuIleSerThrGlnHisAspGluThrVal 201  
QY 680 ACCAAGCAGAAATTCGAGCTGACCTCAAGAGAGCTGTGATCAAGCCGTGATCCGGAG 739  
Db 202 ThrAsnAspGluIleAlaArgAspLeuLysGluHisValIleLysProValIleProGlu 221  
QY 740 AGTACCTTGATGAGAGACCACTTTCACCTTGAACCCCTCTGGCGGTTTGTCTGATGA 799  
Db 222 LysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheValIleGly 241  
QY 800 GGTCTTCAGGCTGATGCTGCTCTCACCGCGCGCAAGATCATCATGATATTCAGGGA 859  
Db 242 GlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleIleAspThrTyrGlyGly 261  
QY 860 TGGGTGCTCATGGTGGTGGTCTCTCCGGAAGGATCCCAAGGTTGATAGGAGT 919  
Db 262 TrpGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSer 281  
QY 920 GGTGCTTACATTTGAGCAGCGCTGTAGACATTTGGCAAGTGGACTACCGAAGG 979  
Db 282 GlyAlaTyrIleValArgGlnAlaAlaLysSerValValAlaAsnGlyMetAlaArg 301  
QY 980 TGCATTGTGCAAGTGTCTTATGCTGTCGCGAGCCCTTGTGCTCTTTGTGAC 1039  
Db 302 AlaLeuValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAsp 321  
QY 1040 ACCTATGGCCCGGGAAGATCCATGATAAGAGATTCTCAACATTTGTGAAGGAACTTT 1099  
Db 322 ThrTyrGluThrGlyLeuIleProAspLysGluIleLeuLysIleValLysGluSerPhe 341  
QY 1100 GATTTGAGCCCGGATGATGATCCATCAACCTTGATCTCAAGAGGGTGGGAATACAGG 1159  
Db 342 AspPheArgProGlyMetMetThrIleAsnLeuAspLeuLysArgGlyGlyAsnGlyThr 361

QY 1160 TTCCTTGAAGACTGCTGCATATCGACACTTCGCAGAGAGACCCCTGACTTCATCGGAA 1219  
Db 362 PheLeuLysThrAlaAlaTyrGlyHisPheGlyArgAspAspProAspPheThrTrpGlu 381  
QY 1220 GTGCTCAGCCCTCAAGTGGGAGAAG 1246  
Db 382 ValValLysProLeuLysTrpAspLys 390

## RESULT 6

T10710

methionine adenosyltransferase (EC 2.5.1.6) - clove pink

NAlternate names: S-adenosylmethionine synthetase

C:Species: Dianthus caryophyllus (clove pink)

C&gt;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004

R:Accession: T10710

R:Larsen, P.B.; Woodson, W.R.

submitted to the EMBL Data Library, April 1991

A:Description: Cloning and nucleotide sequence of a s-adenosylmethionine synthetase cDN

A:Reference number: Z17091

A:Accession: T10710

A&gt;Status: translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-396 &lt;LAR&gt;

A:Cross-references: UNIPROT:P24260; EMBL:M61882; NID:g167961; PID:g304637

C:Genetics:

A:Gene: SAM2

C:Function:

A:Description: catalyzes the formation of S-adenosyl methionine with phosphate and pyro

C:Superfamily: methionine adenosyltransferase

C:Keywords: S-adenosylmethionine; transferase

## Alignment Scores:

Pred. No.:	1-38e-146	Length:	396
Score:	1932.50	Matches:	364
Percent Similarity:	95.90%	Conservative:	10
Best Local Similarity:	93.33%	Mismatches:	15
Query Match:	70.32%	Indels:	1
DB:	2	Gaps:	1

US-10-734-698A-38 (1-1485) x T10710 (1-396)

QY 77 GCAGAGACATTCCTATTACCTCAGAGTCAAGTGAACGAGGACACCTGACAGCTCTGC 136  
Db 5 AlaAspThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCys 24  
QY 137 GACCAATCTCGATGCTGCTCGACGCTTGCCTTGAACAGGACCCAGACAGCAAGTT 196  
Db 25 AspGlnIleSerAspAlaValLeuAspAlaCysLeuAlaGlnAspAlaGluSerLysVal 44  
QY 197 GCCTGCGAAACATGCACCAAGACCAACTTGGTTCATGGTCTTCGGAGAGATCACCAAG 256  
Db 45 AlaCysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThrLys 64  
QY 257 GCCAACGTTGATACGAGAAGATCGTGCCTGACACCTCAGGAAACATCGGCTCTCTCA 316  
Db 65 AlaAsnValAspTyrGluLysIleValAlaAspThrCysArgGluIleGlyPheValSer 84  
QY 317 AACGATGGGACTTGATGCTGACACTGCAAGTCTTGTAAACATTTGACGAGCAGAGC 376  
Db 85 ProAspValGlyLeuAspAlaAspAsnCysLysValLeuValTyrIleGluGlnSer 104  
QY 377 CCTGATATTCAGGGGTGCACGGCCACTTACCAAAAGACCCGAGGAAATCGGTGCT 436  
Db 105 ProAspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluAspIleGlyAla 124  
QY 437 GGAGACCAAGGTCATCATGTTTGGCTTATGCCACGAGCAAAACCCAGAAATTTGATGCCATTG 496  
Db 125 GlyAspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeu 144  
QY 497 AGTCATGTTCTTGCACTAAACTCGGTGCTCTCACCAGGGTTCGCAAGAACCGAACC 556  
Db 145 SerHisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThr 164





QY 980 TGCAATGTCAGTGTCTTATGCAATGTTGGTGTGCCGAGCCTTTGTCTGTCTTTGTGAC 1039  
||||:|||||  
Db 304 CysLeuValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAsp 323  
||||:|||||  
QY 1040 ACCTATGGCACCGGAGATCCATGATAAGGAGATTCTCAACATTGTGAAGGAGAACTTT 1099  
:::|||||  
Db 324 SerTyrGlyThrGlyLysIleProAspArgGluIleLeuAsnIleValLysGluAlaPhe 343  
:::|||||  
QY 1100 GATTTCAGGCCCGGTATGATCTTCATCAACCTTTGATCTCAAGAGGGGTGGGAATAACAGG 1159  
||||:|||||  
Db 344 AspPheArgProGlyMetIleSerIleSerLeuAspLeuLeuArgGlyGlyAsnGlyArg 363  
||||:|||||  
QY 1160 TTC---TTGAAGACTGCTGATATGACACTTCGGCAGACAGGACCTGACTTCACATGG 1216  
||||:|||||  
Db 364 PheLeuLeuLysThrAlaAlaTyrGlyHisPheGlySerAspAlaAspPheThrTrp 383  
||||:|||||  
QY 1217 GAAGTGGTCAAGCCCTC 1234  
||||:|||||  
Db 384 GluValValLysProLeu 389  
||||:|||||

## RESULT 8

T06180

methionine adenosyltransferase (EC 2.5.1.6) - barley

N;Alternate names: S-adenosylmethionine synthetase

C;Species: Hordeum vulgare (Barley)

C;Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 09-Jul-2004

C;Accession: T06180

R;Wori, S.

submitted to the EMBL Data Library, August 1995

A;Reference number: Z15512

A;Accession: T06180

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-394 &lt;MOR&gt;

A;Cross-references: UNIPROT:P50299; EMBL:D63835; PIDN:BAA09895.1

C;Superfamily: methionine adenosyltransferase

C;Keywords: S-adenosylmethionine; transferase

## Alignment Scores:

Pred. No.:	5,04e-144	Length:	394
Score:	1900.50	Matches:	354
Percent Similarity:	96.16%	Conservative:	22
Best Local Similarity:	90.54%	Mismatches:	14
Query Match:	69.16%	Indels:	1
DB:	2	Gaps:	1

US-10-734-698A-38 (1-1485) x T06180 (1-394)

QY 77 GCAGAGACATTCCTATTACCTCAGAGTCAGTGAACGAGGACACCCCTGACAGCTCTGC 136  
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Db 3 AlaGluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCys 22  
||||:|||||  
QY 137 GACCAATCTCCGATGCTCTCTCGAGCGCTTGTGACAGGACCCGACAGCAGGTT 196  
||||:|||||  
Db 23 AspGlnValSerAspAlaValLeuAspAlaCysLeuAlaGlnAspProAspSerLysVal 42  
||||:|||||  
QY 197 GCCTCGCAACATGTCACCAAGACCACTTGCTCATGCTCTTCGAGAGATCACCCCAAG 256  
||||:|||||  
Db 43 AlaCysGluThrCysThrLysThrAsnMetValMetValPheGlyGluIleThrLys 62  
||||:|||||  
QY 257 GCCAACGTTGACTACGAGAGATCGTGCCTGACACTCGAGGAACATCGGCTCGCTCA 316  
||||:|||||  
Db 63 AlaThrValAspTyrGluLysIleValArgAspThrCysArgAspIleGlyPheIleSer 82  
||||:|||||  
QY 317 AACGATGGGACTTGATGCTGCAACTGCAAGTCTCTGTAAACATTGACGACGACGAC 376  
||||:|||||  
Db 83 AspAspValGlyLeuAspAlaAspHisCysLysValLeuValAsnIleGluGlnGlnSer 102  
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QY 377 CCTGATATTGCCAGGGTGTGCACGCGCCACTTTACCAAAAGACCCGAGGAATCGGTGCT 436  
||||:|||||  
Db 103 ProAspIleAlaGlnGlyValHisGlyHisPheThrLysArgProGluGluValGlyAla 122  
||||:|||||  
QY 437 GGAGACGAGGGTGCATGTTTGGCTATGCCACGAGCAAAACCCAGAAATTGATGCCATTG 496  
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Db 123 GlyAspGlnGlyIleMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeu 142  
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QY 497 AGTCATGTTCTTGGCAACTAAACTCGGTGCTCTCACCAGGTTCCGAAGACGCAACC 556  
:::|||||  
Db 143 ThrHisMetLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThr 162  
:::|||||  
QY 557 TCCCATGTTGAGGCTGATCGGAAACCCAAAGTGACTGTTGAGPATTCAATGACAAC 616  
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Db 163 CysAlaTrpLeuArgProAspGlyLysThrGlnValThrIleGluTyrLeuAsnGluGly 182  
||||:|||||  
QY 617 GGTGCCATGTTCCAGTTCGTCTCCACTGTCTATCTCCACCAACCATGATGAGACT 676  
||||:|||||  
Db 183 GlyAlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGluThr 202  
||||:|||||  
QY 677 GTGACCAACGACGAAATTGCAGCTGACCTCAAGGAGCATGTGATCAAGCGGTGATCCCG 736  
||||:|||||  
Db 203 ValThrAsnAspGluIleAlaAspLeuLysGluHisValIleLysProValIlePro 222  
||||:|||||  
QY 737 GAGAACTACCTTGATGAGAAGACCAATTTTCCACTTGAAACCTCTGCGCGTTTGTCAAT 796  
||||:|||||  
Db 223 GlyLysTyrLeuAspGluAsnThrIlePheHisLeuAsnProSerGlyArgPheValIle 242  
||||:|||||  
QY 797 GSAGGTCTCACGGTGATGCTGCTCACCGCGCCGCMAGATCATCATCGATCTTACGGA 856  
||||:|||||  
Db 243 GlyGlyProHisGlyAspAlaGlyLeuThrAlaArgLysIleIleAspThrTyrGly 262  
||||:|||||  
QY 857 GGATGGGTGCTCATGTTGTTGCTTCTCCGGNAGGATCCCAACCAAGGTTGATAGG 916  
||||:|||||  
Db 263 GlyTrpGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArg 282  
||||:|||||  
QY 917 AGTGTGCTTACATTGTGAGACAGCTGCTAAAGACATTGTGCGCAAGTCGACTAGCCAGA 976  
||||:|||||  
Db 283 SerGlyAlaTyrIleAlaArgGlnAlaLysSerIleIleAlaSerGlyLeuAlaArg 302  
||||:|||||  
QY 977 AGGTGCATTGTCAAGTGTCTTATGCCATTGTGTGCCGAGCCTTGTCTGCTTGT 1036  
||||:|||||  
Db 303 ArgCysIleValGlnIleSerTyrAlaIleGlyValProGluProLeuSerValPheVal 322  
||||:|||||  
QY 1037 GACACCTATGGCACCGGGAAGATCCATGATAAGGAGATTCTCAACATTCTGAAGGAGAAC 1096  
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Db 323 AspSerTyrGlyThrGlyLysIleProAspArgGluIleLeuLysValLysGluAsn 342  
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QY 1097 TTTGATTTTCAGCCCGGTATGATCTCCATCAACCTTGATCTCAAGAGGGGTGGGAATAAC 1156  
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Db 343 PheAspPheArgProGlyMetIleThrIleAsnLeuAspLeuLysGlyGly---Asn 361  
||||:|||||  
QY 1157 AGTTCCTTGAAGACTGCTGCATATGACACACTTCCGAGAGAGACCCCTGACTTCATCG 1216  
||||:|||||  
Db 362 ArgPheIleLysThrAlaAlaTyrGlyHisPheGlyArgAspAlaAspPheThrTrp 381  
||||:|||||  
QY 1217 GAAGTGGTCAAGCCCTCAAGTGGGAGAGGCC 1249  
||||:|||||  
Db 382 GluValValLysProLeuLysPheAspLysAla 392  
||||:|||||

## RESULT 9

S46540

methionine adenosyltransferase (EC 2.5.1.6) - tomato

N;Alternate names: S-adenosyl-L-methionine synthetase

C;Species: Lycopersicon esculentum (tomato)

C;Date: 26-Dec-1994 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004

C;Accession: S46540; S38876

R;Espartaco, J.; Pintor-Toro, J.A.; Pardo, J.M.

Plant Mol. Biol. 25, 217-227, 1994

A;Title: Differential accumulation of S-adenosylmethionine synthetase transcripts in re-

A;Reference number: S46538; MUID:94289846; PMID:8018671

A;Accession: S46540

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-390 &lt;ESP&gt;

A;Cross-references: UNIPROT:P43282; EMBL:Z24743; NID:9429107; PIDN:CAA80867.1; PID:94291

C;Superfamily: methionine adenosyltransferase

C;Keywords: S-adenosylmethionine; transferase



Alignment Scores:  
Pred. No.: 1,05e-142 Length: 390  
Score: 1884.00 Matches: 352  
Percent Similarity: 95.34% Conservativeness: 16  
Best Local Similarity: 91.19% Mismatches: 18  
Query Match: 68.56% Indels: 0  
DB: 2 Gaps: 0

US-10-734-698A-38 (1-1485) x S46540 (1-390)

QY 80 GAGACATTCCTATTACCTCAGAGTCAAGAGGAGACCCCTGACAAAGCTCTGCAC 139  
DB 2 GluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCysAsp 21  
QY 140 CAAATCTCCGATGCTGCTCCGAGCTTCCCTTGAACAGGACCCAGACAGCAAGGTTGCC 199  
DB 22 GluValSerAspAlaIleLeuAspAlaCysLeuGluGlnAspProGluSerLysValAla 41  
QY 200 TCGGAACATGCACCAAGACCACTTGGTCATGGTCTTCGGAGAGATCACCAACAGGCC 259  
DB 42 CysGluThrCysThrLysThrAsnMetValPheGlyGluIleThrThrLysAla 61  
QY 260 AACGTTGACTACGAGAAGATCGTGGCTGACACCTGCAGGAAATCGGCTCTCTCAAC 319  
DB 62 ThrValAspTyrGluLysIleValAlaAspThrCysArgGlyIleGlyPheValSerAla 81  
QY 320 GATGGGACTGATGCTGACAACTGCAAGGTCCTTGTAAACATTGAGCAGAGACCCCT 379  
DB 82 AspValGlyLeuAspAlaAspAenCysLysValLeuValAsnIleGluGlnGlnSerPro 101  
QY 380 GATATTGCCAGGCTGTGACCGCCACCTTACCAAGACCCGAGGAATCGGCTCTGGA 439  
DB 102 AspIleAlaGlnGlyValHisGlyHisLeuThrLysLysProGluGluIleGlyAlaGly 121  
QY 440 GACCAAGGTCACATGTTTGGCTATGTCACGAGCAAAACCCAGAAATGATGTCATTGAT 499  
DB 122 AspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuThr 141  
QY 500 CATGTTCTTGCACAACTCCGCTGCTCTCACCGAGTTCGCAAGAACCGAACCTGTC 559  
DB 142 HisValLeuAlaThrLysLeuGlyAlaLysLeuThrGluValArgLysAsnLysThrCys 161  
QY 560 CCATGTTGAGCCCTGATCGGAAACCCCAAGTACTGTTGAGTATTCAATGACACACCGT 619  
DB 162 ProTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrLysAsnAspAsnGly 181  
QY 620 GCATGTTCCAGTTCGCTGTCACACTGTGCTTATCTCCACCCCAACATGATGAGACTGTG 679  
DB 182 AlaMetValProIleArgValHisThrValLeuIleSerThrGlnHisAspGluThrVal 201  
QY 680 ACCAAGCAAGAAATTCAGCTGACCTCAAGAGGACATGATCAAGCCGGTGTATCCGGAG 739  
DB 202 ThrAsnAspGlnIleAlaGlnAspLeuLysGluHisValIleLysProValIleProAla 221  
QY 740 AGTACTTGTAGAGAACCAATTTTCCACTTGAACCCCTCTGGCGGTTTGTCTGATGGA 799  
DB 222 LysTyrLeuAspGluAsnThrIlePheHisLeuAsnProSerGlyArgPheValIleGly 241  
QY 800 GGTCTCTCAGGTGATGCTGCTCTCACCGCCGCAAGATCATCATGATATTCACGAGGA 859  
DB 242 GlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyrGlyGly 261  
QY 860 TGGGCTGCTCATGGTGGTGGTCTTCTCCGGGAAGGATCCCAAGGTTGATGAGGT 919  
DB 262 TrpGlyAlaHisGlyGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSer 281  
QY 920 GGTGCTTACATGTGAGACAGCTGTAGAGCATGTGGCACTGACCTACCGAGAGG 979  
DB 282 GlyAlaTyrIleValArgGlnAlaAlaLysSerValValAlaSerGlyLeuAlaArgArg 301  
QY 980 TGCAATGTCAGAGTGTCTTATGCAATGGTGTGGCCGAGCCCTTGTCTGTTTGTGAC 1039

DB 302 CysIleValGlnValSerTyrAlaIleGlyValAlaGluProLeuSerValPheValAsp 321  
QY 1040 ACCTATGCGCCGCGAGATCCATGATGAAGAGATTTCTCAACATTTGTAAGGAGAACTTT 1099  
DB 322 ThrTyrLysThrGlyThrIleProAspLysAspIleLeuValLeuIleLysGluAsnPhe 341  
QY 1100 GATTTTCAGGCCCGGTGATGATCTCCATCAACCTTGCATCTCAAGAGGGGTGGGAATAACAGG 1159  
DB 342 AspPheArgProGlyMetMetSerIleAsnLeuAspLeuLeuArgGlyGlyAsnTyrArg 361  
QY 1160 TTCTGAAGACTGTCATATGCACATTCGCGAGAGAGGACCCCTGATTCACATGGGAA 1219  
DB 362 TyrGlnLysThrAlaAlaTyrGlyHisPheGlyArgAspAspProAspPheThrTrpGlu 381  
QY 1220 GTGGTCAAGCCCTCAAG 1237  
DB 382 ThrValLysValLeuLys 387

RESULT 10  
GB4785  
probable s-adenosylmethionine synthetase [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C:Accession: G84785  
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Unayam, L.; Tallon, L.;  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487; PMID:10617197  
A:Accession: G84785  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-390 <STO>  
A:Cross-references: UNIPROT:Q9SUL8; GB:AE002093; NID:G4883604; PIDN:AAD31573.1; GSPDB:GN  
C:Gene: At2g36880  
A:Map position: 2  
C:Superfamily: methionine adenosyltransferase

Alignment Scores:  
Pred. No.: 9.64e-142 Length: 390  
Score: 1872.00 Matches: 348  
Percent Similarity: 95.08% Conservativeness: 19  
Best Local Similarity: 90.16% Mismatches: 19  
Query Match: 68.12% Indels: 0  
DB: 2 Gaps: 0

US-10-734-698A-38 (1-1485) x G84785 (1-390)

QY 80 GAGACATTCCTATTACCTCAGAGTCAAGAGGAGACCCCTGACAAAGCTCTGCAC 139  
DB 2 GluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCysAsp 21  
QY 140 CAAATCTCCGATGCTGCTCCGAGCTTCCCTTGAACAGGACCCAGACAGCAAGGTTGCC 199  
DB 22 GluIleSerAspAlaIleLeuAspAlaCysLeuGluGlnAspProGluSerLysValAla 41  
QY 200 TCGGAACATGCACCAAGACCAATTCGTCATGGTCTTCGGAGAGATCACCAACAGGCC 259  
DB 42 CysGluThrCysThrLysThrAsnMetValPheGlyGluIleThrThrAlaAla 61  
QY 260 AACGTTGACTACGAGAAGATCGTGGTGCACACCTGCAGGAAATCGGCTCTCTCAAC 319  
DB 62 LysValAspTyrGluLysIleValArgSerThrCysArgGluIleGlyPheIleSerAla 81  
QY 320 GATGGGACTGATGCTGACAACTGCAAGGTCCTTGTAAACATTGAGCAGAGACCCCT 379  
DB 82 AspValGlyLeuAspAlaAspLysCysAsnValLeuValAsnIleGluGlnGlnSerPro 101  
QY 380 GATATTGCCAGGCTGTGACCGCCACCTTACCAAGACCCGAGGAATCGGCTCTGGA 439  
DB 102 AspIleAlaGlnGlyValHisGlyHisLeuThrLysLysProGluGluIleGlyAlaGly 121

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QY 440 GACACGGGTCAATGTTTGGCTATGACCGACGGAACCCAGAAATTCAGTTCATTCAGT 499
Db 122 AspGlnGlyHisMetPheGlyTyAlaThrAspGluThrProGluLeuMetProLeuThr 141
QY 500 CATGTTCTTGCACAACTCAACTCGGTGCTCGCTCACCAGGTTCCGCAAGAACGCACTGC 559
Db 142 HisValLeuAlaThrLysLeuGlyAlaLysLeuThrGluValArgLysLeuLysThrCys 161
QY 560 CCATGGTTGAGGCTCATGGGAAACCCAAAGTCACTGTTGAGTATTACAAATGCAACAGCT 619
Db 162 ProTyrLeuArgProAspGlyLysThrGlnValThrValGluTyrLysLeuAspGlyGly 181
QY 620 GCCATGGTTCCAGTTCGTGTCACACTGCTTATCTCCACCAACCAATGATGAGACTGTCG 679
Db 182 AlaMetIleProIleArgValHisThrValLeuIleSerThrGlnHisAspGluThrVal 201
QY 680 ACCAAGCAGCAATTCAGCTGACCTCAAGGACATGTCACAGGCGGTGATCAAGCGGTGATCC 739
Db 202 ThrAsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIleProAla 221
QY 740 AAGTACTCTGATGAGAGAACCAATTTCCACTTGAACCCCTCTGCGCGTTCATTCATGGA 799
Db 222 LysTyrLeuAspAsnThrIlePheHisLeuAsnProSerGlyArgPheValIleGly 241
QY 800 GGTCTCACGGTGATGCTGCTCTCACCGGCGCAAGATCATCATCATCTTACCGAGGA 859
Db 242 GlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyrGlyGly 261
QY 860 TGGGGTGCTCATGGTGGTGGTCTTCTCCGGGAGGATCCCAAGGTTGATGAGGTTGATGAG 919
Db 262 TrpGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSer 281
QY 920 GGTGCTTACATTCGAGACAGGCTGCTAAGAGCATTTGCGCAAGTGCAGTACGCAAGG 979
Db 282 GlyAlaTyrIleValArgGlnAlaAlaLysSerValAlaAlaGlyLeuAlaArgArg 301
QY 980 TGCATTGTGCAAGTGTCTTATGTCATTGGTGTGCGCGAGCCTTGTCTGCTTGTGTGAC 1039
Db 302 CysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAsp 321
QY 1040 ACCTATGGCACCGGGAAGATCCATGATAGGAGATTCACACATGTTGAGGAGAACTTT 1099
Db 322 ThrTyrLysThrGlyThrIleProAspLysAspIleLeuValIleLysGluAlaPhe 341
QY 1100 GATTTCAGGCGCGGTATGATCTCCATCAACTTGTATCTCAAGAGGGGTGGGAATAACAG 1159
Db 342 AspPheArgProGlyMetMetAlaIleAsnLeuAspLeuLysArgGlyLysAsnPheArg 361
QY 1160 TTCTTGAAGACTGCTGCATATGACACTTCGGCAGAGAGGACCCCTGACTTCACATGGGAA 1219
Db 362 PheGlnLysThrAlaAlaTyrGlyHisPheGlyArgAspAspProAspPheThrTrpGlu 381
QY 1220 GTGTCACAGCCCTCAAG 1237
Db 382 ValValLysProLeuLys 387

RESULT 11
S49491
methionine adenosyltransferase (EC 2.5.1.6) - garden petunia
C:Species: Petunia x hybrida (garden petunia)
C>Date: 01-Feb-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S49491
R:Izhaki, A.; Shoseyov, O.; Weiss, D.
A:Submitted to the EMBL Data Library, October 1994
A:Description: Petunia cDNA encoding S-Adenosylmethionine synthetase.
A:Reference number: S49491
A:Molecule type: mRNA
A:Residues: 1-390 <I>ZH>
A:Cross-references: UNIPROT:P48498; EMBL:X82214; NID:G559505; PIDN:CAA57696.1; PID:G5595
C:Superfamily: methionine adenosyltransferase
C:Keywords: S-adenosylmethionine; transferase
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Alignment Scores:
Pred. No.: 1.53e-140 Length: 390
Score: 1857.00 Matches: 344
Percent Similarity: 94.81% Conservative: 21
Best Local Similarity: 89.33% Mismatches: 20
Query Match: 67.58% Indels: 0
DB: 2 Gaps: 0

US-10-734-698A-38 (1-1485) x S49491 (1-390)
QY 80 GAGACATTCCTATTTACCTCAGAGTCAGTGAACGAGGACACCTTGACAGCTCTCGGAC 139
Db 2 GluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCysAsp 21
QY 140 CAAATCTCCGATGCTGCTCCTCGACCTTGCCTTGAACAGACCCAGACACCAAGGTTGCC 199
Db 22 GlnValSerAspAlaIleLeuAspAlaCysLeuGluAspProGluSerLysValAla 41
QY 200 TCGAAACATGCAACCAAGACCACTTGTGTCATGCTTCGAGAGATCAACCAAGGCC 259
Db 42 CysGluThrCysThrLysThrAsnMetValMetValPheGlyGluIleThrThrLysAla 61
QY 260 AACGTTGACTACGAGAAGATCGTGTGTCACCTCGACCTGACGAGCAATCGGCTTCGCTCA 319
Db 62 ThrValAspTyrGluLysIleValArgAspThrCysArgGlyIleGlyPheThrSerAla 81
QY 320 GATGTCGACCTTGTGTCACCACTGCAAGGTCCTTGTAAACATTTGAGCAGCAGACCTCT 379
Db 82 AspValGlyLeuAspAlaAspHisCysLysValLeuValAsnIleGluGlnIleSerPro 101
QY 380 GATATTGCCAGGGTGTGCACGGCCACTTACCAAAAGACCCGAGGAAATCGGTCTGGA 439
Db 102 AspIleAlaGlnGlyValHisGlyHisLeuThrLysLysProGluGluIleGlyAlaGly 121
QY 440 GACACGGTCACTGTTGGCTATGCCACGACGAAACCCCGAATTTGATGCTTGCATTCAGT 499
Db 122 AspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuThr 141
QY 500 CATGTTCTTGCACAACTCAACTCGGTGCTCGCTCACCAGGTTTCGCAAGAACGCAACCTGC 559
Db 142 HisValTrpAlaThrLysLeuGlyAlaLysLeuThrGluValArgLysLeuLysThrCys 161
QY 560 CCATGGTTGAGGCTGATGGGAAACCCCAAGTGCATGTTGAGTATTACAAATGCAACAGCT 619
Db 162 ProTyrLeuArgProAspGlyLysThrGlnValThrValGluTyrArgAsnAspGly 181
QY 620 GCCATGGTTCCAGTTCGTGTCACACTGCTTATCTCCACCAACATGATGAGACTGTCG 679
Db 182 AlaMetIleProLeuArgValHisThrIleLeuIleSerThrGlnHisAspGluThrVal 201
QY 680 ACCAAGCAGCAATTCAGCTGACCTCAAGGACATGTCACAGGCGGTGATCAAGCGGTGATCC 739
Db 202 ThrAsnAspGlnIleAlaGlnAspLeuLysGluHisValIleLysProValIleProAla 221
QY 740 AAGTACTCTGATGAGAGAACCAATTTCCACTTGAACCCCTCTGCGCGTTCATTCATGGA 799
Db 222 GluTyrLeuAspGluAsnThrIlePheHisLeuAsnProSerGlyArgPheValIleGly 241
QY 800 GGTCTCACGGTGATGCTGCTCTCACCGGCGCAAGATCATCATCATCTTACCGAGGA 859
Db 242 GlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyrGlyGly 261
QY 860 TGGGGTGCTCATGGTGGTGGTCTTCTCCGGGAGGATCCCAAGGTTGATGAGGTTGATGAG 919
Db 262 TrpGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSer 281
QY 920 GGTCTTACATTCGAGACAGGCTGCTAAGAGCATTTGCGCAAGTGCAGTACGCAAGG 979
Db 282 GlyAlaTyrIleValArgGlnAlaAlaLysSerValAlaAlaGlyLeuAlaArgArg 301
QY 980 TGCATTGTGCAAGTGTCTTATGTCATTGGTGTGCGCGAGCCTTGTCTGCTTGTGTGAC 1039
Db 302 CysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAsp 321
QY 1040 ACCTATGGCACCGGGAAGATCCATGATAGGAGATTCACACATGTTGAGGAGAACTTT 1099
Db 322 ThrTyrLysThrGlyThrIleProAspLysAspIleLeuValIleLysGluAlaPhe 341
QY 1100 GATTTCAGGCGCGGTATGATCTCCATCAACTTGTATCTCAAGAGGGGTGGGAATAACAG 1159
Db 342 AspPheArgProGlyMetMetAlaIleAsnLeuAspLeuLysArgGlyLysAsnPheArg 361
QY 1160 TTCTTGAAGACTGCTGCATATGACACTTCGGCAGAGAGGACCCCTGACTTCACATGGGAA 1219
Db 362 PheGlnLysThrAlaAlaTyrGlyHisPheGlyArgAspAspProAspPheThrTrpGlu 381
QY 1220 GTGTCACAGCCCTCAAG 1237
Db 382 ValValLysProLeuLys 387

RESULT 11
S49491
methionine adenosyltransferase (EC 2.5.1.6) - garden petunia
C:Species: Petunia x hybrida (garden petunia)
C>Date: 01-Feb-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S49491
R:Izhaki, A.; Shoseyov, O.; Weiss, D.
A:Submitted to the EMBL Data Library, October 1994
A:Description: Petunia cDNA encoding S-Adenosylmethionine synthetase.
A:Reference number: S49491
A:Molecule type: mRNA
A:Residues: 1-390 <I>ZH>
A:Cross-references: UNIPROT:P48498; EMBL:X82214; NID:G559505; PIDN:CAA57696.1; PID:G5595
C:Superfamily: methionine adenosyltransferase
C:Keywords: S-adenosylmethionine; transferase
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Db 302 CyslleValGlnValSerTyrAlaIleGlyValAlaGluProLeuSerValPheValAsp 321  
Qy 1040 ACTATGGACCGGAGATCCATATAGAGAGATCTCAACATTTGTGAAGAGAACTTT 1099  
Db 322 ThrTyrLysThrGlyThrLeuProAspLysAspIleLeuThrLeuIleGlyLeuAsnPhe 341  
Qy 1100 GATTTCAGGCGCGGTATGATCTCCATCAACTTGTATCTCAAGAGGGGTGGGAATAACAGG 1159  
Db 342 AspPheArgProGlyMetSerIleAsnLeuAspLeuLysGlyGlyAsnPheArg 361  
Qy 1160 TTCTTTGAAGACTGCTGCATATGGACATTTCCGACAGAGAGCCCTGACTTCCATGGGAA 1219  
Db 362 TyrGlnLysThrAlaAlaTyrGlyHisPheGlyArgAspAspProAspPheThrTrpGlu 381  
Qy 1220 GTGGTCAAGCCCTC 1234  
Db 382 ThrValLysValLeu 386

RESULT 12  
S66351  
methionine adenosyltransferase (EC 2.5.1.6) 1 - garden pea (fragment)  
C:Species: Pisum sativum (garden pea)  
C>Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
C:Accession: S66351  
R:Gomez-Gomez, L.; Carrasco, P.  
Plant Mol. Biol. 30, 821-832, 1996  
A:Title: Hormonal regulation of S-adenosylmethionine synthase transcripts in pea ovaries  
A:Reference number: S66351; MUID:96194463; PMID:8624412  
A:Accession: S66351  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-366 <COM>  
A:Cross-references: UNIPROT:P49612; EMBL:X82076; NID:g609222; PIDN:CAAS7580.1; PID:g6092  
A>Note: the authors did not translate the codon for residue 1  
C:Superfamily: methionine adenosyltransferase  
C:Keywords: S-adenosylmethionine; transferase

Alignment Scores:  
Pred. No.: 3 19e-136 Length: 366  
Score: 1803.00 Matches: 341  
Percent Similarity: 95.33% Conservative: 6  
Best Local Similarity: 93.68% Mismatches: 17  
Query Match: 65.61% Indels: 0  
DB: 2 Gaps: 0

US-10-734-698A-38 (1-1485) x S66351 (1-366)

Qy 158 CTCGACGCTTGCTTGAAACAGGACCCAGACAGAGGTTGCTCGCAACATGCACCAAG 217  
Db 3 ValAspAlaCysLeuGluGlnAspSerAspSerLysValAlaCysGluThrCysThrLys 22  
Qy 218 ACCAATTGGTCATGCTTCGGAGAGATCACACCAAGCCCAACGTTGACTACGAGAAG 277  
Db 23 ThrAsnLeuValMetValPheGlyGluIleThrThrLysAlaAsnValAspTyrGluLys 42  
Qy 278 ATCGTCGTCACCTCGAGGACATCGCTTCGCTCAACAGATGTGGACTTCATGCT 337  
Db 43 IleValArgAsnThrCysArgAsnIleGlyPheValSerAlaAspValGlyLeuAspAla 62  
Qy 338 GACAACTGCAAGTCTCTTAAACATTGAGCAGCAGAGCCCTGATATTGCCCGAGGTGTG 397  
Db 63 AspAsnCysLysValLeuValAsnIleGluGlnInSerProAspIleAlaGlnGlyVal 82  
Qy 398 CACGGCCACTTACCAAAAGACCCGAGGAAATCGGTGTGGAGACAGGTCACATGTTT 457  
Db 83 HisGlyHisPheThrLysLysProGluIleGlyAlaGlyAspGlnGlyHisMetPhe 102  
Qy 458 GGCATGCCACGACCAACCCAGNATTGATGCCATTGAGTCATGTTCTTCCAACTAAA 517  
Db 103 GlyTyrAlaThrAspGluThrProGluLeuMetProLeuSerHisValLeuAlaThrLys 122  
Qy 518 CTCGGTGTCTCTCACCAGGTTTCGCAAGACCGAACTGCGCCATGGTTGAGGCTGAT 577

Db 123 LeuGlyAlaArgLeuThrGluValArgLysAsnGlyThrCysAlaIleTrpLeuArgProAsp 142  
Qy 578 GGGAAACCCCAAGTGAAGTGTGACTATTACATACAAACGTCATGTTCCATGTTGCT 637  
Db 143 GlyAsnThrGlnValThrValGluTyrTyrAsnAspLysGlyAlaMetValProIleArg 162  
Qy 638 GTCCACACTGTGCTTATCTCCACCACATGATGAGACTGTGACCAACGACGAAATTCGA 697  
Db 163 ValHisThrValLeuIleSerThrGlnHisAspGluThrValThrAsnAspGluIleAla 182  
Qy 698 GCTCACTCAAGGAGCATGTGATCAAGCCGGTGTATCCCGAGAGAGTACCTTGTATGAGAAG 757  
Db 183 AlaAspLeuLysGluHisValIleLysProValIleProGluLysTyrLeuAspSerLys 202  
Qy 758 ACCATTTTCCACTTGAACCCCTCTGGCGCTTTTCTCATTTGGAGGTCCTCAGGTGATGCT 817  
Db 203 ThrIleCysHisLeuAsnProSerGlyArgPheValIleGlyGlyProHisGlyAspAla 222  
Qy 818 GGTCTCAACCGCCGCAAGATCATCATCTACTTACGGAGGATGGGTGCTCATGGTGGT 877  
Db 223 GlyLeuThrGlyArgLysIleIleAspThrTyrGlyGlyTyrGlyAlaHisGlyGly 242  
Qy 878 GGTCTTTCTCCGGAAGGATCCCAAGGATTCACCAAGGTTGATAGAGTGTGCTTACATTTGAGA 937  
Db 243 GlyAlaPheSerGlyLysAspProThrLysValAspArgArgGlyAlaTyrIleValArg 262  
Qy 938 CAGCTCTAAGACATTTGGCAAGTGGACTAGCAGGAGGTCATTTGTCACAGTGTCT 997  
Db 263 GlnAlaLysSerIleValAlaSerGlyLeuAlaArgArgAlaIleValGlnLeuLeu 282  
Qy 998 TATGCAATTGGTGGCCGAGCCTTTGCTCTCTTTTGTGACCTATGCGACCCGGGAAG 1057  
Db 283 ArgAlaIleGlyValProGluProLeuSerValPheValAspThrTyrGlyThrGlyLys 302  
Qy 1058 ATCCATGATAAGGAGATTCCTCAACATTTGTGAAGGAGAACATTTGATTTTCAGGCCCGGTATG 1117  
Db 303 IleProAspArgGluIleLeuLysIleValLysGluThrPheAspPheArgProGlyMet 322  
Qy 1118 ATCTCCATCAACCTTGATCTCAAGGGGTGGGATAACAGGTTCTTGAAGCATGCTCA 1177  
Db 323 IleSerIleAsnLeuAspLeuLeuArgGlyGlyAsnGlyArgPheLeuLysThrAlaAla 342  
Qy 1178 TATGGACACTTCGCGCAGAGAGACCTTGACTTCATGTCATGCGGAAGTGGTCAAGCCCTCAAG 1237  
Db 343 TyrGlyHisPheGlyArgGluAspProAspPheThrTrpGluValValLysProLeuLys 362

Qy 1238 TGGGAGAGGCC 1249  
Db 363 TrpGluLysAla 366

RESULT 13  
T06592  
methionine adenosyltransferase (EC 2.5.1.6) - garden pea (fragment)  
C:Species: Pisum sativum (garden pea)  
C>Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 05-May-2000  
C:Accession: T06592  
R:Gomez, L.; Carrasco, P.  
submitted to the EMBL Data Library, January 1995  
A:Description: Hormonal regulation of the S-adenosylmethionine synthase in pea ovaries.  
A:Reference number: 215782  
A:Accession: T06592  
A>Status: preliminary; translated from GB/EMBL/DBBJ  
A:Molecule type: mRNA  
A:Residues: 1-360 <COM>  
A:Cross-references: EMBL:LJ3680; NID:g609556; PIDN:AAAS8772.1; PID:g609557  
C:Superfamily: methionine adenosyltransferase  
C:Keywords: S-adenosylmethionine; transferase

Alignment Scores:  
Pred. No.: 2 45e-131 Length: 360  
Score: 1742.00 Matches: 335  
Percent Similarity: 93.13% Conservative: 4  
Best Local Similarity: 92.03% Mismatches: 19

Query Match:	63.39%	Indels:	6
DB:	2	Gaps:	1
US-10-734-698A-38 (1-1485) x T06592 (1-360)			
QY	158	CTCGACGCTTGGCTTGAACAGGACCCAGACAGCAAGGTGGCTCGCAAAATGCACCAAG	217
DB	3	ValAspAlaCysLeuGluGlnAspSerAspSerLysValAlaCysGluThrCysThrLys	22
QY	218	ACCAACTTGGTCATGCTCTTCGAGAGATCACCAAGGCCAACCTTCAGTACGAGAAG	277
DB	23	ThrAsnLeuValMetValPheGlyGluThrThrLysAlaAsnValAspTyrGluLys	42
QY	278	ATCGTCGGTGACACCTCGAGGAACATCGGCTTCTCAACGATGTGGACATTGATGCT	337
DB	43	IleValArgAsnThrCysArgAsnIleGlyPheValSerAlaAspValGlyLeuAspAla	62
QY	338	GACAACCTGAAGTCTCTTGAACATTGAGCAGCAGACCCCTCATATTCGCCAGGTGG	397
DB	63	AspAsnCysLysValLeuValAsnIleGluGlnGlnSerProAspIleAlaGlnGlyVal	82
QY	398	CACGGCCACCTTACCAAAAGACCCGAGAAATCGGTGCTGGAGACCAAGGTACATGTTT	457
DB	83	HisGlyHisPheThrLysArgProGluGluIleGlyAlaGlyAspGlnGlyHisMetPhe	102
QY	458	GGCTATGCCACGGAACGAAACCCAGAAATTGATGCCATTGAGTCATGTTCTTGCAATAA	517
DB	103	GlyTyrAlaThrAspGluThrProGluLeuMetProLeuSerHisValLeuAlaThrLys	122
QY	518	CTCGGTCTGCTCACCGAGTTCGCAAGACCGACCTGCCCATCGTTGAGGCTGAT	577
DB	123	LeuGlyAlaArgLeuThrGluValArgLysAsnGlyThrCysAlaThrLeuArgProAsp	142
QY	578	GGGAAACCAAGTACTGTAGTATTACAATGACAAACGGTGCCATGTTCCAGTTCGT	637
DB	143	GlyAsnThrGlnValThrValGluTyrTyrAsnAspLysGlyAlaMetValProIleArg	162
QY	638	GTCCACACTGTGCTTATCTCCACCCCAACATGATGAGACTGTGACCAACGACGAAATGCA	697
DB	163	ValHisThrValLeuIleSerThrGlnHisAspGluThrValThrAsnAspGluIleAla	182
QY	698	GCTGACCTCAAGAGCATGTGATCAACCGCGTGATCCCGAGAGTACCTTGATGAGAG	757
DB	183	AlaAspLeuLysGlyHisValIleLysProValIleProGluLysTyrLeuAspSerLys	202
QY	758	ACCATTTTCCACTTGAACCCCTCTGCGCTTTTGTTCATTGGAGGTCTCACGCTGATGCT	817
DB	203	ThrIlePheHisLeuAsnProSerGlyArgPheValIleGlyProHisGlyAspAla	222
QY	818	GGTCTCACCGCGCGCAAGATCATCATCTTACGAGAGATGGGGTGCTCATGTTGCT	877
DB	223	GlyLeuThrGlyArgLysIleIleAspThrTyrGlyCysThrArgCys-----	239
QY	878	GGTGCTTCTCCGGGAAGATCCACCAAGTTGTATAGAGTGGTGCTTACATTGTGAGA	937
DB	240	-----SerGlyLysAspProThrLysValAspArgArgGlyAlaTyrIleValArg	256
QY	938	CAGGCTGCTTAAGAGCATTTGGCAAGTGGACTAGCCAGAGGTGCATTGTGCAAGTGCT	997
DB	257	GlnAlaAlaLysSerIleValAlaSerGlyLeuAlaArgArgAlaIleValGlnValSer	276
QY	998	TATGCCATTGGTGTGCCGAGCCTTTGTCTGTTTGTGTTGACACCTATGGCCCGGGAAG	1057
DB	277	TyrAlaIleGlyValProGluProLeuSerValPheValAspThrTyrGlyThrGlyLys	296
QY	1058	ATCCATGATAAGAGATTCTCAACATTGTGAAGGAGAACTTGAATTCAGGCCCGGTATG	1117
DB	297	IleProAspArgGluIleLeuLysIleValLysGluThrPheAspPheArgProGlyMet	316
QY	1118	ATCTCCATCAACTCTCAAGAGGGGTGGCAATAACAGGTTCTTTGAAGACTGTGCA	1177
DB	317	IleSerIleAsnLeuAspLeuArgGlyGlyAsnGlyArgPheLeuLysThrAlaAla	336

QY	1178	TATGACACTTCGGCAGAGAGACCCCTGACTTCACATGCGGAAGTGGTCAAGCCCTCAAG	1237
DB	337	TyrGlyHisPheGlyArgGluAspProAspPheThrTrpGluValValLysProLeuLys	356
QY	1238	TGGGAGAGGCC	1249
DB	357	TrpGluLysAla	360
RESULT 14			
S27257			
methionine adenosyltransferase (EC 2.5.1.6) 2 alpha chain - human			
N.Alternate names: renal methionine adenosyltransferase (MAT); S-adenosylmethionine syn-			
C.Species: Homo sapiens (man)			
C.Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004			
C.Accession: S27257			
R.Horikawa, S.; Tsukada, K.			
FEBS Lett. 312, 37-41, 1992			
A.Title: Molecular cloning and developmental expression of a human kidney S-adenosylmet-			
A.Reference number: S27257; M01D:93050159; PMID:1426236			
A.Accession: S27257			
A.Status: preliminary			
A.Molecule type: mRNA			
A.Residues: 1-395 <HOR>			
A.Cross-references: UNIPROT:P31153; EMBL:X68036; GB:S47059; NID:g36326; PIDN:CAA48726.1,			
C.Genetics:			
A.Gene: GDB:MAT2A; SAMS2; MATA2			
A.Cross-references: GDB:136213; OMIM:601468			
A.Map position: 2p11.2-2p11.2			
A.Introns: 15/2; 256/3			
C.Complex: heterodimer of catalytic alpha and regulatory beta chains			
C.Function:			
A.Description: catalyzes the formation of S-adenosyl methionine with phosphate and pyro-			
A.Pathway: one-carbon metabolism			
C.Superfamily: methionine adenosyltransferase			
C.Keywords: ATP; heterodimer; kidney; magnesium; metalloprotein; one-carbon metabolism;			
F.279-286/Region: nucleotide-binding motif A (P-loop) #status atypical			
F.31/Binding site: magnesium 2 (Asp) #status predicted			
F.285,289/Active site: Lys #status predicted			
F.291/Binding site: magnesium 1 (Asp) #status predicted			
Alignment Scores:			
Pred. No.:	3,11e-97	Length:	395
Score:	1316.50	Matches:	254
Percent Similarity:	78.50%	Conservative:	49
Best Local Similarity:	65.80%	Mismatches:	76
Query Match:	47.91%	Indels:	7
DB:	1	Gaps:	3
US-10-734-698A-38 (1-1485) x S27257 (1-395)			
QY	83	ACATTCTCTATTACCTCAGATCAGTGAACGAGGACACCCCTGACAAAGCTCTGCGACCAA	142
DB	17	ThrPheLeuPheThrSerGluSerValGlyGluGlyHisProAspLysValCysAspGln	36
QY	143	ATCTCCGATGCTGCTCTCGACGCTTGTGAACAGGACCCAGACAGCAAGTTGCTGCTGC	202
DB	37	IleSerAspAlaValLeuAspAlaHisLeuGlnGlnAspProAspAlaLysValAlaCys	56
QY	203	GAACATGCCACCAAGACCAACTTGGTCATGCTTCGCGAGAGATCACCACCAAGGCCAAC	262
DB	57	GluThrValAlaLysThrGlyMetIleLeuLeuAlaGlyGluIleThrSerArgAlaAla	76
QY	263	GTTGACTACGAGAAGATCGTGCATCACACCTGCAGAACATCGGCTTGTCTCTCAACCGAT	322
DB	77	ValAspTyrGlnLysValValArgGluAlaValLysHisIleGlyTyrAspAspSerSer	96
QY	323	GTGGACCTTGATGCTGACCACTGCAAGGTCTTGTAAACATTGACAGCAGACCCCTGAT	382
DB	97	LysGlyPheAspTyrLysThrCysAsnValLeuValAlaLeuGluGlnGlnSerProAsp	116
QY	383	ATTGCCAGGCTGTGCACGGCCACTTACCAAAAGACCCGAGGAATCGTCTCGAGAC	442
DB	117	IleAlaGlnGlyVal-----HisLeuAspArgAsnGluGluAspIleGlyValAlaGlyAsp	134

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QY 443 CAGGTCACATCTTTGGCTATGCCCGGACGAAACCCAGATTTGATGCCATTTGAGTCAT 502
Db 135 GlnGlyLeuMetPheGlyTyrAlaThrAepGluThrGluGluCysMetProLeuThrIle 154
QY 503 GTTCTTGCAACTAAACTCGGTGCTGCTCTCACCGAGGTTCCGAAAGAAAGCACTTCGCCA 562
Db 155 ValLeuAlaHisLysLeuAsnAlaLysLeuAlaGluLeuArgArgAsnGlyThrLeuPro 174
QY 563 TGGTTGAGCCTGATGGGAAACCCCAAGTACTGTTTGAGTATTACAATGACAAACGGTGCC 622
Db 175 TrpLeuArgProAspSerLysThrGlnValThrValGlnTyrMetGlnAspArgGlyAla 194
QY 623 ATGGTTCCAGTTGCTGTCACACTGTCTTATCTCACCCACCAACATGATGAGTCTGACC 682
Db 195 ValLeuProIleArgValHisThrIleValIleSerValGlnHisAspGluValCys 214
QY 683 AACGACGAATTCGACCTGACCTCAAGGAGCATGTGATCAAGCCGGTATCCCGGAGAAG 742
Db 215 LeuAspGluMetArgAspAlaLeuLysGluLysValIleLysAlaValProAlaLys 234
QY 743 TACCTTGATGAGAAGACCAATTTCCACTTGAACCCCTCTGCGCGTTTGTCTATTGGAGGT 802
Db 235 TyrLeuAspGluAspThrIleTyrHisLeuGlnProSerGlyArgPheValIleGlyGly 254
QY 803 CCTCAGGTGATGCTGCTCACCGCCGCAAGATCATCATCATCTTACGAGGATGG 862
Db 255 ProGlnGlyAspAlaGlyLeuThrGlyArgLysIleValAspThrTyrGlyGlyTyr 274
QY 863 GTGTGCTCATGTTGCTGCTTCTCCGGGAAGGATCCCAAGGTTTGTATAGGAGTGT 922
Db 275 GlyAlaHisGlyGlyAlaPheSerGlyLysAspTyrThrLysValAspArgSerAla 294
QY 923 GCTTACATTTGTGAGACAGCTGCTAAGACATTTGGCAAGTGGAGTACTAGCCAGAGTGC 982
Db 295 AlaTyrAlaAlaArgTrpValAlaLysSerLeuValLysGlyGlyLeuCysArgVal 314
QY 983 ATTTGTCAGTGTCTTATCCCATTTGGTGCCGAGCCTTCTGCTCTTTGTCACACC 1042
Db 315 LeuValGlnValSerTyrAlaIleGlyValSerHisProLeuSerIleSerIlePheHis 334
QY 1043 TATGCAACCCGGAAGATCCATGATAGGAGATTCTCAACATTTGTGAAGGAGAACTTTGAT 1102
Db 335 TyrGlyThrSerGlnLysSerGluArgGluLeuLeuGluLeuValLysLysAsnPheAsp 354
QY 1103 TTCAGCCCGGTATGATCTCCATCAACTTGTATCTCAAGAGGGGTGGGAATTAACAGTTC 1162
Db 355 LeuArgProGlyValIleValArgAspLeuAspLeuLysLys-----ProIleTyr 371
QY 1163 TTGAAGACTGCTGCATATGCACATCTCGGACAGAGGACCTTGACTTCACATGGGAGTGT 1222
Db 372 GlnArgThrAlaAlaTyrGlyHisPheGlyArgAsp-----SerPheProTrpGluVal 389
QY 1223 GTCAAGCCCTCAAGTGG 1240
Db 390 ProLysLysLeuLysTyr 395
RESULT 15
A37118
methionine adenosyltransferase (BC 2.5.1.6) - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 15-Feb-1991 #sequence_revision 15-Feb-1991 #text_change 09-Jul-2004
C:Accession: A37118
R:Horikawa, S.; Sasuga, J.; Shimizu, K.; Ozasa, H.; Tsukada, K.
J. Biol. Chem. 265, 13683-13686, 1990
A:Title: Molecular cloning and nucleotide sequence of cDNA encoding the rat kidney s-ade
A:Reference number: A37118, MUID:90337979, PMID:1696256
A:Accession: A37118
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-395 <HOR>
A:Cross-references: UNIPROT:P182298; GB:J05571; NID:g206845; PID:AAA42106.1; PID:g206846
C:Superfamily: methionine adenosyltransferase
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C;Keywords: S-adenosylmethionine; transferase

Alignment Scores: 9.41e-97 Length: 395  
Pred. No.: 1310.50 Matches: 251  
Score: 78.24% Conservative: 51  
Best Local Similarity: 65.03% Mismatch: 77  
Query Match: 47.69% Indels: 7  
Gaps: 3

US-10-734-698A-38 (1-1485) x A37118 (1-395)

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QY 83 ACATTCTTATTACTCTCAGAGTCAGTGAACGAGGACACCCCTGACAGCTCTGGACCAA 142
Db 17 ThrPheLeuPheThrSerGluSerValGlyGluGlyHisProAspLysIleCysAspGln 36
QY 143 ATCTCCGATGCTGCTCTGACGCTTGGCTTGAACAGAGCCAGACAGCAAGTTGCTTCGC 202
Db 37 IleAsnAspAlaValLeuAspAlaHisLeuGlnGlnAspProAspAlaLysValAlaCys 56
QY 203 GAAACATGCACCAAGACCACTTGGTCATGCTCTCGAGAGATCACCAACGAGCCCAAC 262
Db 57 GluThrValAlaLysThrGlyMetIleLeuLeuAlaGlyGluIleThrSerArgAlaAla 76
QY 263 GTTGACTACGAGAAGATCGTCGTGACACCTGACAGGAACATCGGCTTCTCAACACCAT 322
Db 77 IleAspTyrGlnLysValValArgGluAlaIleLysHisIleGlyTyrAspAspSerSer 96
QY 323 GTGGACTTGTGATGTCACACTGCAAGGCTCTTGTAAACATGTAGACGACGAGCCCTGAT 382
Db 97 LysGlyPheAspTyrLysThrCysAsnValLeuValAlaLeuGluGlnGlnSerProAsp 116
QY 383 ATTCGCCAGGTGTCACGCGCCACTTACCAAAAGACCCGAGGAATCGGTCTGGAGAC 442
Db 117 IleAlaGlnGlyVal-----HisLeuAspArgAsnGluLeuAspIleGlyAlaGlyAsp 134
QY 443 CAGGTCACATGTTTGGCTATGCCACGACGACAAACCCAGAAATTTGATGCCATTTGAGTCAT 502
Db 135 GlnGlyLeuMetPheGlyTyrAlaThrAspGluThrGluGluCysMetProLeuThrIle 154
QY 503 GTTCTTGCAACTAAACTCGGTGCTGCTCTCACCGAGGTTTCGAAAGAAAGCACTTCGCCA 562
Db 155 ValLeuAlaHisLysLeuAsnAlaLysLeuAlaGluLeuArgArgAsnGlyThrLeuPro 174
QY 563 TGGTTGAGCCTGATGGGAAACCCCAAGTACTGTTTGAGTATTACAATGACAAACGGTGCC 622
Db 175 TrpLeuArgProAspSerLysThrGlnValThrValGlnTyrMetGlnAspArgGlyAla 194
QY 623 ATGGTTCCAGTTGCTGCTCACACTGCTTATCTCCACCCCAACATGATGAGACTGTGACC 682
Db 195 ValIleProIleArgValHisThrIleValIleSerValGlnHisAspGluValCys 214
QY 683 AACGACGAATTTGACGATGACCTCAAGGAGCATGTGATCAAGCCGGTATCCCGGAGAAG 742
Db 215 LeuAspGluMetArgAspAlaLeuLysGluLysLeuIleLysAlaValProAlaLys 234
QY 743 TACCTTGATGAGAAGACCAATTTCCACTTGAACCCCTCTGCGCGTTTGTCTATTGGAGGT 802
Db 235 TyrLeuAspGluAspThrIleTyrHisLeuGlnProSerGlyArgPheValIleGlyGly 254
QY 803 CCTCAGGTGATGCTGCTCTCACCGCCGCAAGATCATCATCATCTTACGAGGATGG 862
Db 255 ProGlnGlyAspAlaGlyLeuThrGlyArgLysIleValAspThrTyrGlyGlyTyr 274
QY 863 GTGTGCTCATGTTGCTGCTTCTCCGGGAAGGATCCCAAGGTTTGTATAGGAGTGT 922
Db 275 GlyAlaHisGlyGlyAlaPheSerGlyLysAspTyrThrLysValAspArgSerAla 294
QY 923 GCTTACATTTGTGAGACAGCTGCTAAGACATTTGGCAAGTGGAGTACTAGCCAGAGTGC 982
Db 295 AlaTyrAlaAlaArgTrpValAlaLysSerLeuValLysGlyGlyLeuCysArgVal 314
QY 983 ATTTGTCAGTGTCTTATCCCATTTGGTGCCGAGCCTTCTGCTCTTTGTCACACC 1042
```



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GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: August 25, 2005, 17:02:27 ; Search time 276.5 Seconds

(without alignments)  
5500.453 Million cell updates/sec

Title: US-10-734-698A-38

Perfect score: 2748

Sequence: 1 AGCCAGGCCCACTCAACCA.....CAAAAGAAATGTTCCAAAGTT 1485

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5

Ygapop 10.0, Ygapext 0.5

Fgapop 6.0, Fgapext 7.0

Delop 6.0, Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DRV=xlp  
-Q/cn2\_1/USPTO spool\_p/US10734698/runat\_25082005\_105400\_10267/app.query.fasta\_1.1671  
-DB=Uniprot -QFMT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10734698 @CN 1 1 307 @runat\_25082005\_105400\_10267 -NCPU=6 -ICPU=3  
-NO\_WMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG  
-DRV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Uniprot 03:\*

1: uniprot\_sprot:\*

2: uniprot\_treml:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2035	74.1	392	Q8W3Y4	Phaseolus lunatus (lima bean) (Phaseolus limensis).
2	2007	73.0	391	Q6JXK6	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
3	2003	72.9	393	Q6JXK6	OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
4	2003	72.9	393	Q6JXK6	OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
5	1993	72.5	393	Q9AT55	OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
6	1992	72.5	393	Q9AT55	OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
7	1989	72.4	395	Q9AT56	OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
8	1986	72.3	393	Q84NM2	OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
9	1985	72.2	393	Q84NM2	OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
10	1983	72.2	393	Q84NM2	OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
11	1979	72.0	393	Q9SBQ7	OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
12	1974.5	71.9	395	Q944U4	OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
13	1972.5	71.8	429	Q8GTL5	OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
14	1968	71.6	393	Q6GV10	OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
15	1960	71.3	393	Q9FUZ1	OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
16	1959	71.3	395	Q9FPL6	OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

17	1957.5	71.2	394	1	METL_ORYSA	P93438 oryza sativ
18	1957.5	71.2	394	1	Q7F660	Q7F660 oryza sativ
19	1953	71.1	396	1	METK_ORYSA	P46611 oryza sativ
20	1953	71.1	396	2	Q6AVZ2	Q6AVZ2 oryza sativ
21	1952	71.0	393	2	Q94FA4	Q94FA4 brassica ju
22	1949	70.9	396	2	Q8VXC5	Q8VXC5 oryza sativ
23	1949	70.9	396	2	Q9LGU6	Q9LGU6 oryza sativ
24	1948.5	70.9	396	2	Q6F3F0	Q6F3F0 arabidopsis
25	1947	70.9	393	1	METL_ARATH	P17562 arabidopsis
26	1940.5	70.6	392	1	METK_MESCR	P93254 mesembryant
27	1940	70.6	393	1	METK_ARATH	P23586 arabidopsis
28	1940	70.6	393	2	Q94FA6	Q94FA6 brassica ju
29	1939.5	70.6	396	2	Q6F3F1	Q6F3F1 arabidopsis
30	1938	70.5	393	2	Q9LDQ7	Q9LDQ7 camellia si
31	1935.5	70.4	396	2	Q6F3F4	Q6F3F4 arabidopsis
32	1935	70.4	393	2	Q9LUT2	Q9LUT2 dianthus ca
33	1932.5	70.3	396	1	METL_DIACA	P24260 dianthus ca
34	1932	70.3	393	1	METK_BRAJU	P49611 brassica ju
35	1931.5	70.3	393	1	METK_MUSAC	Q22338 musa acumin
36	1930.5	70.3	396	2	Q7XZRI	Q7XZRI atriplex nu
37	1926.5	70.1	396	2	Q6F3F3	Q6F3F3 atriplex nu
38	1907	69.4	393	1	METK_PINBN	P50300 pinus banks
39	1906	69.4	393	2	Q9FVQ7	Q9FVQ7 pinus conto
40	1900.5	68.2	394	1	METM_HORVU	P50299 hordeum vul
41	1884	68.6	390	1	METM_LYCBS	P43282 lycopersico
42	1872	68.1	390	2	Q9S7L8	Q9S7L8 arabidopsis
43	1869	68.0	390	2	Q9M7K8	Q9M7K8 nicotiana t
44	1866	67.9	390	2	Q94FA5	Q94FA5 brassica ju
45	1857	67.6	390	1	METK_PETHY	P48498 petunia hyb

#### ALIGNMENTS

RESULT 1  
Q8W3Y4 PRELIMINARY; PRT; 392 AA.  
AC Q8W3Y4;  
DT 01-MAR-2002 (TREMELrel. 20, Created)  
DT 01-MAR-2002 (TREMELrel. 20, Last sequence update)  
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)  
DE S-adenosylmethionine synthetase.  
GN Name=SAMS;  
OS Phaseolus lunatus (lima bean) (Phaseolus limensis).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.  
OX NCBI\_TaxID=3884;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22056020; PubMed=12060229;  
RA Arimura G., Ozawa R., Nishioka T., Boland W., Koch T., Kuhnemann F.,  
RA Takabayashi J.;  
RT "Herbivore-induced volatiles induce the emission of ethylene in  
neighboring lima bean plants.";  
RL Plant J. 29:87-98(2002).  
CC -|- FUNCTION: Catalyzes the formation of S-adenosylmethionine from  
methionine and ATP (By similarity).  
CC -|- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +  
diphosphate + S-adenosyl-L-methionine.  
CC -|- COFACTOR: Binds 2 divalent ions, such as magnesium or cobalt, and  
1 potassium ion per subunit (By similarity).  
CC -|- PATHWAY: Activated methyl cycle.  
CC -|- SIMILARITY: Belongs to the AdoMet synthetase family.  
DR EMBL; AB062358; BAB83761.1; -;  
DR HSSP; F13444; 1QM4.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0000287; F:magnesium ion binding; IEA.  
DR GO; GO:0004478; F:methionine adenosyltransferase activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0006730; P:one-carbon compound metabolism; IEA.  
DR Pfam; PF02773; S-AdoMet\_synt\_C; 1.  
DR Pfam; PF02772; S-AdoMet\_synt\_M; 1.  
DR Pfam; PF00438; S-AdoMet\_synt\_N; 1.

DR PIRSF: PIRSF000497; MAT: 1.  
 DR TIGRFAMs: TIGR01034; metK; 1.  
 DR PROSITE: PS00376; ADOMET\_SYNTHETASE\_1; 1.  
 DR PROSITE: PS00377; ADOMET\_SYNTHETASE\_2; 1.  
 KW ATP-binding; Magnesium; Metal-binding; One-carbon metabolism;  
 KW Potassium; Transference.  
 SQ SEQUENCE 392 AA; 43060 MW; 9F4CA2CAAD240209 CRC64;

Alignment Scores:  
 Pred. No.: 2,17e-149 Length: 392  
 Score: 2035.00 Matches: 384  
 Percent Similarity: 98.72% Conservativity: 5  
 Best Local Similarity: 97.96% Mismatches: 5  
 Query Match: 74.05% Indels: 0  
 DB: 2 Gaps: 0

US-10-734-698a-38 (1-1485) x Q8W3Y4 (1-392)

QY 74 ATGGCAGAGACATTCCTATTTACCTCAGATCAGTGAACGAGGGACACCCCTGACAGCTC 133  
 Db 1 MetAlaGluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeu 20

QY 134 TCGCACCAATCTCCGATCTCTCTCCGACGCTTGCCTTTGAACAGGACCCACAGCAAG 193  
 Db 21 CysAspGlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProGluSerLys 40

QY 194 GTTGCTGCGAAACATGACCAAGACCAACTGCTGTCATGGCTTCGGAGAGATCACACC 253  
 Db 41 ValAlaCysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThr 60

QY 254 AAGGCCAAGCTTGACTACGAGAGAGATCGTGGCTGACCTCGCAGGAACATCGCTTCGTC 313  
 Db 61 LysAlaAsnValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheIle 80

QY 314 TCAACAGATGTGGACTTGATGCTGACAACTCAAGTCTTGTGTAAACATTTGACGACGAG 373  
 Db 81 SerAsnAspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGlnGln 100

QY 374 AGCCCTGATTTGCCAGGGTGTGCACGGCCACCTTACCAAAAGACCCGAGGAATCGGT 433  
 Db 101 SerProAspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGly 120

QY 434 GCTGGAGACCGGTCACATGTTGGCTATGCGACGAGCAACCCAGAAATTTGATGCCA 493  
 Db 121 AlaGlyAspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetPro 140

QY 494 TTGAGTCATGTTCTTGCAACTAACTCGGTGCTGCTCTCACCGAGTTTCGCAAGAACGGA 553  
 Db 141 LeuSerHisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGly 160

QY 554 ACTGCGCCATGTTGAGGCTGATGGGAAACCCAGAGTACTGTTGAGTATTACATGAC 613  
 Db 161 ThrCysSerTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnAsp 180

QY 614 AACGGTGCCATGTTCCAGTTCGTGCCACTGTCTTATCTCCACCCCAACATCATGAG 673  
 Db 181 LysGlyAlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGlu 200

QY 674 ACTGTGACCAACGAGAAATTCAGCTGACCTCAAGGAGCATGTGATCAAGCCGGTGATC 733  
 Db 201 ThrValThrAsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIle 220

QY 734 CCGGAGAAGTACTTGATGAGAAGACCATTTCCACTTGAACCCCTCTGGCCGCTTTGTC 793  
 Db 221 ProGluLysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheVal 240

QY 794 ATTGAGGTCCTCACGGTCATGCTGCTCTCACCGCGCAAGATCATCATCATCTTAC 853  
 Db 241 IleGlyGlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleLeuAspThrTyr 260

QY 854 GGAGATGGGGTCTCATGGTGGTGGTCTTTCTCGGGAAGGATCCCAACCAAGTTGAT 913  
 Db 261 GlyGlyTyrGlyAlaHisGlyGlyGlyAlaPheSerGlyLysAspProThrLysValaAsp 280

QY 914 AGGAGTGTGCTTACATTGTGAGACAGCTGCTAAGACATTGTGCAAGTGGACTAGCC 973  
 Db 281 ArgSerGlyAlaTyrIleValArgGlnAlaAlaLysSerIleValAlaSerGluLeuAla 300

QY 974 AGAAGGTGCATTGTGCAAGTGTCTTATGCCATTGTGTGCCGAGCCCTTTCTGTCTTT 1033  
 Db 301 ArgArgCysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPhe 320

QY 1034 GTTGACACCTATGGCACCAGGAGATCATGATGAAGAGATTCTCAACATTGTGAAGGAG 1093  
 Db 321 ValAspThrTyrGlyThrGlyLysIleProAspLysGluIleLeuLysIleValValGlu 340

QY 1094 AACTTGTATTTACGCCCGGTATGATCTCCATCACTTGTGATCTCAAGAGGGTGGGAAT 1153  
 Db 341 AsnPheAspPheArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyLysAsn 360

QY 1154 AACAGGTTCTTGAAGACTGCTGCATATGGACACTTCGGCAGAGAGCCCTGACTTCACA 1213  
 Db 361 SerArgPheLeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThr 380

QY 1214 TGGGAAGTGTGCAAGCCCTCAAGTGGGAGAGGCC 1249  
 Db 381 TrpGluValValLysProLeuLysTrpGluLysAla 392

RESULT 2

QY Q6J9X6 PRELIMINARY; PRT; 391 AA.  
 AC Q6J9X6;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE S-adenosylmethionine synthase (Fragment).  
 OS Medicago sativa (Alfalfa).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosids;  
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.  
 ON NCBI\_taxID=3879;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RA Cheng R.M., Carbajal L., Potenza C., Bagga S., Sengupta-Gopalan C.;  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Catalyzes the formation of S-adenosylmethionine from  
 methionine and ATP (By similarity).  
 CC -!- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +  
 diphosphate + S-adenosyl-L-methionine.  
 CC -!- COFACTOR: Binds 2 divalent ions, such as magnesium or cobalt, and  
 1 potassium ion per subunit (By similarity).  
 CC -!- PATHWAY: Activated methyl cycle.  
 CC -!- SIMILARITY: Belongs to the AdoMet synthetase family.  
 DR EMBL; AY560003; AY40304.1; -. IEA.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0000287; F:magnesium ion binding; IEA.  
 DR GO; GO:0004478; F:methionine adenosyltransferase activity; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0006730; P:one-carbon compound metabolism; IEA.  
 DR InterPro; IPR002133; S-AdoMet\_synth.  
 DR Pfam; PF02773; S-AdoMet\_synth\_C; 1.  
 DR Pfam; PF02772; S-AdoMet\_synth\_M; 1.  
 DR Pfam; PF00438; S-AdoMet\_synth\_N; 1.  
 DR PIRSF; PIRSF000497; MAT; 1.  
 DR TIGRFAMs; TIGR01034; metK; 1.  
 DR PROSITE; PS00376; ADOMET\_SYNTHETASE\_1; 1.  
 DR PROSITE; PS00377; ADOMET\_SYNTHETASE\_2; 1.  
 KW ATP-binding; Magnesium; Metal-binding; One-carbon metabolism;  
 KW Potassium; Transference.  
 FT NON TER 391 391  
 SQ SEQUENCE 391 AA; 42805 MW; 0A1DB416F59C6DCF CRC64;

Alignment Scores:  
 Pred. No.: 3.26e-147 Length: 391  
 Score: 2007.00 Matches: 379  
 Percent Similarity: 97.95% Conservativity: 3

Best Local Similarity: 97.18%		Matches: 8	
Query Match: 73.03%		Indels: 0	
DB: 2		Gaps: 0	
US-10-734-698A-38 (1-1485) x Q6J9X6 (1-391)			
QY	80	GAGACATTCCTATTACCTCAGAGTCAGTGAACGAGGACACCTCTGACAGCTCTGGAC	139
DB	2	GluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCysAsp	21
QY	140	CAATCTCCGATCGTCTCTCGACGCTTGCTTGAACAGGACCCACGACGACGAGTTGCC	199
DB	22	GlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspValAspSerLysValAla	41
QY	200	TGCGAAACATGCACCAAGACCACTTGGTCATGCTTCGGAGAGATCACCAAGGCC	259
DB	42	CysGluThrCysThrLysThrAsnMetValMetValPheGlyGluIleThrThrLysAla	61
QY	260	AACGTTGATACGAGAAGATCGTGTGTGACACCTCGAGGAACATCGGCTTCGTCTCAAC	319
DB	62	LysValAspTyrGluLysIleValArgAspThrCysArgLysIleGlyPheValSerAsp	81
QY	320	GATGTGGACTGATCTGACACTGCAAGTCTTGTAAACATTCAGCAGCAGACCCCT	379
DB	82	AspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGlnSerPro	101
QY	380	GATATTGCCAGGCTGTGCACGGCCACCTTACCAAGACCCGAGGAAATCGGTGCTGA	439
DB	102	AspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGlyAlaGly	121
QY	440	GACCAGGGTCATGTTGGCTATGCCACGAGCAAAACCCAGAAATGTGATTCATGAGT	499
DB	122	AspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuSer	141
QY	500	CATGTTCTTGCACTAACTCGTGTCTCTCACCGAGGTCGCAAGAACCGACCTCGC	559
DB	142	HisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThrCys	161
QY	560	CCATGTTGAGGCTGATGGGAAACCCCAAGTACTGTTGAGTATTACATGACACCGGT	619
DB	162	ProTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrThrAsnAspGly	181
QY	620	GCCATGTTCCAGTTCGTGTCCACACTGTGCTTATCTCCACCAACATGATGAGCTGTG	679
DB	182	AlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGluThrVal	201
QY	680	ACCAAGACGAATTCAGCTGACCTCAGGAGCATGTGATCAAGCCGTGATCCCGAG	739
DB	202	ThrAsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIleProGlu	221
QY	740	AAGTACTCTGATGAGAGACCACTTTCCACTTGAACCCCTCTGGCCGTTTGTCTATTGA	799
DB	222	LysTyrLeuAspSerLysThrIlePheHisLeuAsnProSerGlyArgPheValIleGly	241
QY	800	GTCTCTCAGGTGATCTGCTCTCACCGCCGCAAGATCATCATGATCTTACGAGGA	859
DB	242	GlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyrGlyGly	261
QY	860	TGGGGTGTCTCATGGTGTGCTTCTCCGGGAGGATCCCAACAGTTGATAGAGT	919
DB	262	TrpGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSer	281
QY	920	GTGCTTACATGTGAGACAGGCTGCTAAGAGCATTTGCGCAAGTGCATGACCAAGG	979
DB	282	GlyAlaTyrIleValArgGlnAlaAlaLysSerIleValAlaSerGlyLeuAlaArg	301
QY	980	TGCATGTCCAAGTGTCTTATGCCATTTGTCGCCGAGCCCTTGTCTGCTTTGTTGAC	1039
DB	302	CysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAsp	321
QY	1040	ACCTATGGACCGGAGAGATCATGATAGGAGATCTCAACATTTGTGAGGAGACTTT	1099
DB	322	ThrTyrGlyThrGlyLysIleProAspLysGluIleLeuAsnIleValLysGlnAsnPhe	341

QY 1100 GATTTCCAGCCCGGTATGATCTCCATCAACCTTGATCTCAAGAGGGGTGGGAATACAGG 1159

DB 342 AspPheArgProGlyMetIleSerIleAsnLeuAspLeuLeuArgGlyGlyAsnGlyArg 361

QY 1160 TTCTTGAAGACTGCTGCATATGACACTTCGCGACAGAGGACCCCTGACTTCACATCGGAA 1219

DB 362 PheLeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspAlaAspPheThrTrpGlu 381

QY 1220 GTGGTCAAGCCCTCAAGTGGGAGAGGCC 1249

DB 382 ValValLysProLeuLysTrpGluLysAla 391

RESULT 3

METK CATRO

ID METK CATRO STANDARD; PRT; 393 AA.

AC Q96551;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE S-adenosylmethionine synthetase 1 (EC 2.5.1.6) (Methionine adenosyltransferase 1) (AdoMet synthetase 1).

GN Name=SAMS1;

OS Catharanthus roseus (Rosa periwinkle) (Madagascar periwinkle).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;

OC lamids; Gentianales; Apocynaceae; Rauvolfioideae; Vinceae;

OC Catharanthus.

OX NCBI\_TaxID=4058;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=9718855; PubMed=9037140; DOI=10.1023/A:1005711720930;

RA Schroeder G., Eichel J., Breinig S., Schroeder J.;

RT "Three differentially expressed S-adenosylmethionine synthetases from Catharanthus roseus: molecular and functional characterization.";

RL Plant Mol. Biol. 33:211-222(1997).

CC -!- FUNCTION: Catalyzes the formation of S-adenosylmethionine from methionine and ATP.

CC -!- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate + diphosphate + S-adenosyl-L-methionine.

CC -!- COFACTOR: Binds 2 divalent ions, such as magnesium or cobalt, and 1 potassium ion per subunit (By similarity).

CC -!- PATHWAY: Activated methyl cycle.

CC -!- SIMILARITY: Belongs to the AdoMet synthetase family.

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CC -----

DR EMBL; Z71271; CA959556.1; -.

DR HSSP; P13444; 1QM4.

DR InterPro; IPR002133; S-AdoMet synt.

DR Pfam; PF02773; S-AdoMet synt\_C; 1.

DR Pfam; PF02772; S-AdoMet synt\_M; 1.

DR Pfam; PF00438; S-AdoMet synt\_N; 1.

DR PIRSF; PIRSF000497; MAT; 1.

DR TIGRFAMs; TIGR01034; metK; 1.

DR PROSITE; PS00376; ADOMET SYNTHETASE 1; 1.

DR PROSITE; PS00377; ADOMET SYNTHETASE 2; 1.

DR ATP-binding; Magnesium; Metal-binding; Multigene family; One-carbon metabolism; Potassium; Transferrase.

KW NP\_BIND 119 124 ATP (Potential).

FT METAL 17 17 Magnesium (By similarity).

FT METAL 43 43 Potassium (By similarity).

FT METAL 271 271 Potassium (By similarity).

FT METAL 279 279 Magnesium (By similarity).

FT BINDING 147 147 ATP (Potential).

SQ SEQUENCE 393 AA; 43050 MW; 04371F2B55BE386F CRC64;

## Alignment Scores:

Pred. No.: 6,69e-147 Length: 393  
 Score: 2003.00 Matches: 374  
 Percent Similarity: 98.72% Conservative: 11  
 Best Local Similarity: 95.90% Mismatches: 5  
 Query Match: 72.89% Indels: 0  
 DB: 1 Gaps: 0

US-10-734-698A-38 (1-1485) x METL\_CATRO (1-393)

QY 80 GAGACATCTCTATTACCTCAGAGTCAGTGAACGAGGACACCTCGACAAGCTCTCGCAC 139  
 Db 2 GluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspGlyLeuGlyAsp 21  
 QY 140 CAAATCTCGATGCTGCTCTCAGCGCTTCCTTGAACAGGACCCAGACAGAGGTTGCC 199  
 Db 22 GinIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerIysValAla 41  
 QY 200 TCGAAACATGCACCAAGACCAACTTGGTCATGGTCTTCGGAGAGATCACCAACAGGCC 259  
 Db 42 CysGluThrCysThrIysThrAsnMetValMetValPheGlyGluLeuThrThrIysAla 61  
 QY 260 AACGTTGACTACGAGAAGATCGTGCATGACCTGCAGGAACATCGGCTTCGTCTCAAC 319  
 Db 62 ThrValAspTyrGluIysIleValArgAspThrCysArgSerIleGlyPheValSerAsp 81  
 QY 320 GATGCGGACTGATGCTGACAACTGCAAGGTCCTTGTAAACATTTGAGCAGCAGACGCT 379  
 Db 82 AspValGlyLeuAspAlaAspAsnCysIysValLeuValAsnIleGluGlnGlnSerPro 101  
 QY 380 GATATTGCCAGGCTGTCACGCGCACCTTACCAAGACCCGAGGAATCGTGCTGA 439  
 Db 102 AspileAlaGlnGlyValHisGlyHisLeuThrIysArgProGluGluIleGlyAlaGly 121  
 QY 440 GACCAAGGTCACATGTTTGGCTATGCCAGCAGCAAAACCCAGAAATTTGATGCTATGAT 499  
 Db 122 AspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluPheMetProLeuSer 141  
 QY 500 CATGTTCTTGCATAAATCTGGTGCTGCTCTCAGCGAGTTTCGCAAGAACCGAACCTGCG 559  
 Db 142 HisValLeuAlaThrIysLeuGlyAlaArgLeuThrGluValArgIysAsnGlyThrCys 161  
 QY 560 CATGTTGTCAGGCTGATCGGAAACCCCAAGTACTGTTGAGTATTACAAATCACACCGT 619  
 Db 162 ProTrpLeuArgProAspGlyIysThrGlnValThrValGluTyrTrpAsnGluAsnGly 181  
 QY 620 GCCATGGTTCCAGTTCGTGTCCACACTGTGCTTATCTCCACCAACATGATGAGACTGTG 679  
 Db 182 AlaMetValProValArgValHisThrValIleSerThrGlnHisAspGluThrVal 201  
 QY 680 ACCAAGCAGAAATTCAGCTGACCTCAAGGAGCATGTGATCAAGCCGCTGATCCGGAG 739  
 Db 202 ThrAsnAspGlnIleAlaAlaAspLeuIysGluHisValIleAspProValIleProGlu 221  
 QY 740 AAGTACTTGTGAGAGAACCATTTTCCACTTGAACCCCTCTGCGGCTTTGCTCATTTGA 799  
 Db 222 LysTyrLeuAspGluArgThrIlePheHisLeuAsnProSerGlyArgPheValIleGly 241  
 QY 800 GGTCTCTCAGCGTATGCTGCTCTCACCGCCGCGCAAGATCATCATCTTACGAGGA 859  
 Db 242 GlyProHisGlyAspAlaGlyLeuThrGlyArgGlyIleIleAspThrTyrGlyGly 261  
 QY 860 TGGGCTGCTCATGGTGGTGGTCTTCTCCGGGAAGGATCCACCAAGTTGATAGGAGT 919  
 Db 262 TrpGlyAlaHisGlyGlyAlaPheSerGlyIysAspProThrIysValAspArgSer 281  
 QY 920 GTGCTTACATTTGTGAGACAGGCTGCTAAGAGCATTGTGCGAAGTGCATGACGAGAG 979  
 Db 282 GlyAlaTyrIleValArgGlnAlaAlaIysSerIleValAlaAsnGlyLeuAlaArgArg 301  
 QY 980 TGCATTGTCAAGTGTCTTATGCAATTTGTCGTCGCCGAGCCTTTGCTCTTGTGAC 1039  
 Db 302 CysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAsp 321

QY 1040 ACCTATGCGCACCGGAGAGATCCATGATAAGGAGATTCTCAACATTTGTGAAGGAGACTTT 1099  
 Db 322 ThrTyrGlyThrGlyIysIleProAspIysGluIleLeuIysIleValIysGluAsnPhe 341  
 QY 1100 GATTTCAAGCCCGGTATGATCTCCATCAACCTTGATCTCTCAAGAGGGGTGGGAATAACAGG 1159  
 Db 342 AspPheArgProGlyMetIleAlaIleAsnLeuAspLeuIysArgGlyGlySerGlyArg 361  
 QY 1160 TTCTTGAAGATCTGTCATATGACATTCGCGCAGAGAGGACCCCTGACTTCACATGGGAA 1219  
 Db 362 PheLeuIysThrAlaAlaTyrGlyHisPheGlyArgAspProAspPheThrTrpGlu 381  
 QY 1220 GTGCTCAAGCCCTCAAGTGGGAGAGGCC 1249  
 Db 382 ValValIysProLeuIysTrpGluIysAla 391  
 RESULT 4  
 METL\_CATRO STANDARD; PRT; 393 AA.  
 ID METL\_CATRO  
 AC Q96552;  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DE S-adenosylmethionine synthetase 2 (EC 2.5.1.6) (Methionine  
 adenosyltransferase 2) (AdoMet synthetase 2).  
 GN Name=SMS2;  
 OS Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC lamiales; Gentianales; Apocynaceae; Rauvolfioideae; Vinceae;  
 OC Catharanthus  
 OX NCBI\_TaxID=4058;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97189555; PubMed=9037140; DOI=10.1023/A:1005711720930;  
 RA Schroeder G., Eichel J., Breinig S., Schroeder J.;  
 RT "Three differentially expressed S-adenosylmethionine synthetases from  
 Catharanthus roseus: molecular and functional characterization.";   
 RL Plant Mol. Biol. 33:211-222(1997).  
 CC -!- FUNCTION: Catalyzes the formation of S-adenosylmethionine from  
 methionine and ATP.  
 CC -!- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +  
 diphosphate + S-adenosyl-L-methionine.  
 CC -!- COFACTOR: Binds 2 divalent ions, such as magnesium or cobalt, and  
 1 potassium ion per subunit (by similarity).  
 CC -!- PATHWAY: Activated methyl cycle.  
 CC -!- SIMILARITY: Belongs to the AdoMet synthetase family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (see <http://www.isb-sib.ch/announce/>)  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch).  
 CC -----  
 CC EMBL; Z71272; CAA95857.1; -.  
 DR HSSP; P13444; 1QW4.  
 DR InterPro; IPR002133; S-AdoMet\_synt.  
 DR Pfam; PF02773; S-AdoMet\_synt\_C; 1.  
 DR Pfam; PF02772; S-AdoMet\_synt\_M; 1.  
 DR Pfam; PF0438; S-AdoMet\_synt\_N; 1.  
 DR FIRSF; FIRSF000497; MAT; 1.  
 DR TIGRFAMs; TIGR01034; metK; 1.  
 DR PROSITE; PS00376; ADOMET SYNTHETASE 1; 1.  
 DR PROSITE; PS00377; ADOMET SYNTHETASE 2; 1.  
 KW ATP-binding; Magnesium; Metal-binding; Multigene family;  
 KW One-carbon metabolism; Potassium; Transferase.  
 FT NP\_BIND 119 124 ATP (Potential).  
 FT METAL 17 17 Magnesium (by similarity).  
 FT METAL 43 43 Potassium (by similarity).  
 FT METAL 271 271 Potassium (by similarity).

FT METAL 279 279 Magnesium (By similarity).  
 SQ BINDING 147 147 ATP (Potential).  
 ST SEQUENCE 393 AA; 43004 MW; 4A9070FB5B9B783D CRC64;

## Alignment Scores:

Pred. No.: 6,59e-147 Length: 393  
 Score: 2003.00 Matches: 376  
 Percent Similarity: 98.71% Conservative: 8  
 Best Local Similarity: 96.66% Mismatches: 5  
 Query Match: 72.89% Indels: 0  
 DB: 1 Gaps: 0

US-10-734-698A-38 (1-1485) x METL\_CATRO (1-393)

QY 80 GAGACATTCCTATTACCTCAGAGTCAGTCAACAGGAGACACCTCACAAGCTCTCGGAC 139  
 Db 2 GluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCysAsp 21  
 QY 140 CAAATCTCCGATGCTCTCTCGAGGCTTCGCTTGAACAGGACCCACAGACAGAGTTGCC 199  
 Db 22 GinileSerAspAlaValLeuAspAlaCysLeuAlaGlnAspProGluSerLysValAla 41  
 QY 200 TGGAAACATGCACCAAGACCACTTGGTCATGCTCTCGAGAGATCCACCAAGGCC 259  
 Db 42 CysGluThrCysThrLysThrAsnMetValMetValPheGlyGluIleThrLysAla 61  
 QY 260 AAGCTTGACTACGAGAAATCGTGCCTGACACCTCGAGGAAACATCGCTCTCAAC 319  
 Db 62 GlnValAspTyrGluLysIleValArgAspThrCysArgAlaIleGlyPheValSerAsp 81  
 QY 320 GATGTGGACTGATCTGACAACTGCAAGTCTTGTAAACATTAAGCAGAGAGCCCT 379  
 Db 82 AspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGlnSerPro 101  
 QY 380 GATATTGCCAGGCTGTCAGCGCCACCTTACCARAAGACCCGAGGAATCGTGTGCA 439  
 Db 102 AspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluIleGlyAlaGly 121  
 QY 440 GACCAGGGTCACATGTTTGGCTATGCCAGGACGAAACCCCAAGATTCATGCTAGT 499  
 Db 122 AspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuSer 141  
 QY 500 CATGTTCTTGCAACTAACTCGTGTCTCTCACCGAGTTCGCAAGAACGACCTGC 559  
 Db 142 HisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThrCys 161  
 QY 560 CCATGTTGAGGCTGATCGGAAACCCCAAGTCTGTTGAGTATTACATCAACAGCT 619  
 Db 162 ProThrLeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnAspAsnGly 181  
 QY 620 GCCATGTTCCAGTTCGTCACACTGTCTTATCTCCACCAACATCATGAGACTGTG 679  
 Db 182 AlaMetValProIleArgValHisThrValLeuIleSerThrGlnHisAspGluThrVal 201  
 QY 680 ACAACGAGAAATTCGACTGACCTCAAGAGAGATGATCAAGCCGCTGATCCCGAG 739  
 Db 202 ThrAsnAspGluIleAlaAspLeuLysGluHisValIleLysProValValProGlu 221  
 QY 740 AAGTACTTGTATCAGAGACCACTTTCCACTTGAACCCCTCGCGTTTCTCATTCGA 799  
 Db 222 LysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheValIleGly 241  
 QY 800 GGTCTCTCAGGTCATGCTGCTCTCACCGCCGCAAGATCATCATCATCTTACGAGGA 859  
 Db 242 GlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleIleAspThrThrGlyGly 261  
 QY 860 TGGGTGTCATGTCGTGGTGTCTTCTCCGGAAGGATCCCAAGGTTGATAGGAGT 919  
 Db 262 TrpGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSer 281  
 QY 920 GGTGCTTACATTCGTGAGAGAGCTGTAGAGCATTTGTCGCAAGTGCATACGAGAG 979  
 Db 282 GlyAlaTyrIleValArgGlnAlaAlaLysSerIleValAlaSerGlyLeuAlaArg 301

QY 980 TGCATTGTGCAAGTGTCTTATGCCATTGGTGTGCCGAGCCCTTGTCTGTCTTGTGAC 1039  
 Db 302 CysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAsp 321  
 QY 1040 ACCTATGCCACCGGAAGATCCATGAAGAGATCTCAACATTTGTGAGGAGACTTT 1099  
 Db 322 ThrTyrGlyThrGlyLysIleProAspLysGluIleLeuLysValIleValLysGluAsnPhe 341  
 QY 1100 GATTTTCAGCCCGGTATGATCTCCATCAACCTTGTATCTCAAGAGGGTGGGAATAACAGG 1159  
 Db 342 AspPheArgProGlyMetIleAlaIleAsnLeuAspLeuLysArgGlyGlyAsnSerArg 361  
 QY 1160 TTCTTGAAGACTGTCATATGCACATTCGCGAGAGAGCCCTGACTTCACATGGGAA 1219  
 Db 362 PheLeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThrTrpGlu 381  
 QY 1220 GTGGTCAAGCCCTCAAGTGGGAGAG 1246  
 Db 382 ValValLysProLeuLysPheGluLys 390

RESULT 5  
 Q9AT55 PRELIMINARY; PRT; 393 AA.  
 AC Q9AT55;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE S-adenosyl-L-methionine synthetase (EC 2.5.1.6).  
 GN Name=SAMS2;  
 OS Elaeagnus umbellata (Autumn olive).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids I; Rosales; Elaeagnaceae; Elaeagnus.  
 OX NCBI\_TaxID=43233;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Root node;  
 RA Lee S., An C.;  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Catalyzes the formation of S-adenosylmethionine from methionine and ATP (By similarity).  
 CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate + diposphatate + S-adenosyl-L-methionine.  
 CC -1- COFACTOR: Binds 2 divalent ions, such as magnesium or cobalt, and 1 potassium ion per subunit (By similarity).  
 CC -1- PATHWAY: Activated methyl cycle.  
 CC -1- SIMILARITY: Belongs to the AdoMet synthetase family.  
 DR EMBL; AF346306; AAK29410.1; -;  
 DR HSSP; P13444; 1QM4.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:000287; F:magnesium ion binding; IEA.  
 DR GO; GO:0004478; F:methionine adenosyltransferase activity; IEA.  
 DR GO; GO:0036740; F:transferase activity; IEA.  
 DR GO; GO:0006730; P:one-carbon compound metabolism; IEA.  
 DR InterPro; IPR002133; S-AdoMet\_synth.  
 DR Pfam; PF02773; S-AdoMet\_synth\_M; 1.  
 DR Pfam; PF02772; S-AdoMet\_synth\_N; 1.  
 DR Pfam; PF00438; S-AdoMet\_synth\_N; 1.  
 DR PIRSF; PIRSF000497; MAT; 1.  
 DR TIGRFAMs; TIGR01034; metK; 1.  
 DR PROSITE; PS00376; ADOMET SYNTHETASE 1; 1.  
 DR PROSITE; PS00377; ADOMET SYNTHETASE 2; 1.  
 KW ATP-binding; Magnesium; Metal-binding; One-carbon metabolism;  
 KW Potassium; Transferase;  
 SQ SEQUENCE 393 AA; 43136 MW; CCF8237D70415D4C CRC64;

## Alignment Scores:

Pred. No.: 4,01e-146 Length: 393  
 Score: 1993.00 Matches: 371  
 Percent Similarity: 98.46% Conservative: 12  
 Best Local Similarity: 95.37% Mismatches: 6  
 Query Match: 72.53% Indels: 0

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DB:                2                Gaps:                0
US-10-734-698A-38 (1-1485) x Q9AT55 (1-393)

QY 80 GAGACATTCCTATTACCTCAGAGTGAACGAGGGACACCCTGACAAAGCTCTGCGAC 139
Db 2 GluThrPheLeuPheThrSerGluSerValAenGluGlyHisProAspAspLysLeuCysAsp 21
QY 140 CAAATCTCCGATGCTGCTCCTCAGCGCTTGCCTTGAACAGGACCCGACGACGAGGTGCTGCC 199
Db 22 GlnIleSerAspAlaValLeuAspAlaCysLeuAlaGlnAspProAspSerLysValAla 41
QY 200 TGGGAACATGCACCAAGACCAACTTGGTCATGGTCTTCGGAGAGATCACCAAGGAC 259
Db 42 CysGluThrCysSerLysThrAenMetValPheGlyGluIleThrThrLysAla 61
QY 260 AAGCTTGACTACGAGAAAGATCGTGCCTGACACCTCGCAGGAACATCGCTCTCAAC 319
Db 62 AenValAspTyrGluLysIleValArgAspThrCysArgThrIleGlyPheValSerAsp 81
QY 320 GATGTGGGACTGATCTGCTGACAACTGCAAGGTCTTGTAAACATTTGAGCAGAGCCCT 379
Db 82 AspValGlyLeuAspAlaAspAenCysLysValLeuValAenIleGluGlnSerPro 101
QY 380 GATATTGCCAGGCTGTGCACGCCACCTTACCAGAAAGACCCGAGGAATCGGTGCTGA 439
Db 102 AspIleAlaGlnGlyValHisGlyHisPheThrLysArgProGluIleGlyAlaGly 121
QY 440 GACCAGGGTCACATGTTGGCTATGCCAGCGACGAAACCCCAAGAAATTTGATGCTTGA 499
Db 122 AspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuSer 141
QY 500 CATGTTCTTGCAACTAACTCGGTGCTGCTCCTCAGCGAGTTCGCAAGAACGACCTGCG 559
Db 142 HisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAspGlyThrCys 161
QY 560 CATGTTGTCAGGCTCATCGGAAACCCCAAGTGACTGTTGAGTATTACAATCACAACGCT 619
Db 162 ProTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrTrpAsnAspLysGly 181
QY 620 GCCATGGTTCAGTTCGTGTCACACTGTGCTTATCTCCACCAACATGATGAGACTGTG 679
Db 182 AlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGluThrVal 201
QY 680 ACCAAGCAGAAATTCGACTGACCTCAGGAGCATGTCATCAAGCCGTGATCCCGAG 739
Db 202 ThrAsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValValProGlu 221
QY 740 AAGTACCTTGATGAGAGACCACTTTTCCACTTGAACCCCTCTGCGCTTTGTCATTGGA 799
Db 222 LysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheValIleGly 241
QY 800 GGTCTCTCAGCGTGATGCTGCTCCTCAGCGCCGCAAGATCATCATGACTTTACGAGGA 859
Db 242 GlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleIleAspThrThrGlyGly 261
QY 860 TGGGTGCTCATGTGCTGCTGCTTCTCCGGAGAGGATCCACCAAGTTGATAGGAGT 919
Db 262 TrpGlyAlaHisGlyGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSer 281
QY 920 GTGCTTACATTTGTGAGACAGGCTGCTAAGAGCATTTGTGCGCAAGTGGACTACGAGAGG 979
Db 282 GlyAlaTyrIleValArgGlnAlaAlaLysSerIleValAlaAsnGlyLeuAlaArg 301
QY 980 TGCATTGTGCAAGTGCTTTATGCCATTTGGTGTGCCCGAGCTTTGTCTGCTTGTGTGAC 1039
Db 302 CysIleValGlnValSerTyrAlaIleGlyValProAspProLeuSerValPheValAsp 321
QY 1040 ACCTATGGCACCGGAGAGATCATGATAAGGAGATCTCAACATCTGTGAGGAGACTTT 1099
Db 322 SerTyrGlyThrGlyLysIleProAspLysGluIleLeuLysIleValLysGluAsnPhe 341
QY 1100 GATTTTCAGGCGCGGTATGATCTCCATCAACCTTGATCTCAAGAGGGGTGGGAATAACAGG 1159

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Db 342 AspPheArgProGlyMetIleThrIleAsnLeuAspLeuLysArgGlyGlyAsnAspArg 361
QY 1160 TTCTTGAAGACTGCTGCATATGCACATTCGCGAGAGAGGACCCCTGACTTCACATGGGAA 1219
Db 362 PheLeuLysThrAlaAlaTyrGlyHisPheGlyArgAspAspProAspPheThrTrpGlu 381
QY 1220 GTGCTCAGCCCTCAGTGGGGAAG 1246
Db 382 IleValLysProLeuLysTrpGluLys 390

RESULT 6
Q9AT56
ID Q9AT56 PRELIMINARY; PRT; 393 AA.
AC Q9AT56;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE S-adenosyl-L-methionine synthetase (EC 2.5.1.6).
GN Name=SMS1;
OS Elaeagnus umbellata (Autumn olive).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Rosales; Elaeagnaceae; Elaeagnus.
OX NCBI_taxID=43233;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=Root node;
RA Lee S., An C.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Catalyzes the formation of S-adenosylmethionine from
CC methionine and ATP (by similarity).
CC -!- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
CC diphosphate + S-adenosyl-L-methionine.
CC -!- COFACTOR: Binds 2 divalent ions, such as magnesium or cobalt, and
CC 1 potassium ion per subunit [by similarity].
CC -!- PATHWAY: Activated methyl cycle.
CC -!- SIMILARITY: Belongs to the AdoMet synthetase family.
DR EMBL; AF346305; AAK29409.1; -.
DR HSSP; PI3444; IQM4.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0000287; P:magnesium ion binding; IEA.
DR GO; GO:0004478; P:methionine adenosyltransferase activity; IEA.
DR GO; GO:0016740; P:transferase activity; IEA.
DR GO; GO:0006730; P:one-carbon compound metabolism; IEA.
DR InterPro; IPR002133; S-AdoMet_synt.
DR Pfam; PF02773; S-AdoMet_synt_C; 1.
DR Pfam; PF00438; S-AdoMet_synt_N; 1.
DR PIRSF; PIRSF000497; MAT; 1.
DR TIGRFAMs; TIGR01034; metK; 1.
DR PROSITE; PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE; PS00377; ADOMET_SYNTHETASE_2; 1.
KW ATP-binding; Magnesium; Metal-binding; One-carbon metabolism;
KW Potassium; Transferase.
SQ SEQUENCE 393 AA; 43096 MW; E6DFFD2A9FAD2347 CRC64;

Alignment Scores:
Pred. No.: 4.8e-146 Length: 393
Score: 1992.00 Matches: 371
Percent Similarity: 98.20% Conservative: 11
Best Local Similarity: 95.37% Mismatches: 7
Query Match: 72.49% Indels: 0
DB: Gaps: 2

US-10-734-698A-38 (1-1485) x Q9AT56 (1-393)

QY 80 GAGACATTCCTATTACCTCAGAGTGAACGAGGGACACCCTGACAAAGCTCTGCGAC 139
Db 2 GluThrPheLeuPheThrSerGluSerValAenGluGlyHisProAspAspLysLeuCysAsp 21
QY 140 CAAATCTCCGATGCTGCTCCTCAGCGCTTGCCTTGAACAGGACCCGACGACGAGGTGCTGCC 199

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Db 22 GlnIleSerAspAlaValLeuAaspAlaCysLeuAlaGlnAaspProAspSerLysValAla 41  
QY 200 TGGCAAACTGCACCAAGACCAACTTGGTCATGGTCTTCGGAGAGATCAACCAAGGCC 259  
Db 42 CysGluThrCysSerLysThrAsnMetValMetValPheGlyGluIleThrThrLysAla 61  
QY 260 AAGCTTGACTACAGAGATCGTCGTGACACCTGCAGGAAACATCGCTTCTCAAC 319  
Db 62 AsnValAspTyrGluLysIleValArgAspThrCysArgAlaIleGlyPheValSerAsp 81  
QY 320 GATGTGGGACTTCATGCTGCAACCTGCAAGTCTCTGTAAACATTCAGCAGCAGACCTT 379  
Db 82 AspValGlyLeuAaspAlaAspAsnCysLysValLeuValAsnIleGluGlnSerPro 101  
QY 380 GATATTGCCAGGCTGTGACCGCCACCTTTACAAAAGACCCGAGGAAATCGGTGTGGA 439  
Db 102 AspIleAlaGlnGlyValHisGlyHisPheThrLysArgProGluGluIleGlyAlaGly 121  
QY 440 GACCAGGTCATGTTTGGCTATGCCACGAGCAAAACCCAGAAATTCATTCAGT 499  
Db 122 AspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluTyrMetProLysSer 141  
QY 500 CATGTTCTTCACTAACTCGTGTCTGCTCCACGAGTTCGCAAGAACCGAACCTCG 559  
Db 142 HisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThrCys 161  
QY 560 CATGTTGAGGCTGATGGGAAACCCCAAGTGACTGTTGAGTATTCAATCAACACGCT 619  
Db 162 ProTyrLeuArgProAspGlyLysThrGlnValThrValGluTyrThrAsnGluAsnGly 181  
QY 620 GCATGTTCCAGTTCGTGTCACACTGTGCTTATCTCCACCAACATGATGAGACTGTG 679  
Db 182 AlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGluThrVal 201  
QY 680 ACCAAGCAGCAATTCAGCTGACCTCAAGGAGCATGTATCAAGCCGCTGATCCCGAG 739  
Db 202 ThrAsnAspGluIleAlaAspLeuLysGluHisValIleLysProValIleProGlu 221  
QY 740 AAGTACTCTTGATGAGAGACCATTTTCCACTTGAACCCCTCTGCGCGTGTTCATTTGA 799  
Db 222 LysTyrLeuAaspGluLysThrIlePheHisLeuAaspProSerGlyArgPheValIleGly 241  
QY 800 GTCTCTCAGGTCATGCTGCTCTCACCGCGCAAGATCATCATCATCTTACGAGGA 859  
Db 242 GlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleIleAspThrTyrGlyGly 261  
QY 860 TGGGTCGTCATGCTGCTGCTCTTCTCGGAGAGATCCCAACGAGTTCATAGGACT 919  
Db 262 TrpGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSer 281  
QY 920 GGTGCTTACATTTGAGACAGGCTGCTAAGAGCATTTGTGCAAGTTCGACTAGCCAGG 979  
Db 282 GlyAlaTyrIleValArgGlnAlaLysSerIleValAlaAsnGlyLeuAlaArgArg 301  
QY 980 TGCAATGTGCAAGTGTCTTATGCAATGTGTGCGCGAGCCCTTGTCTGCTTGTGTGAC 1039  
Db 302 CysLeuValGlnValSerTyrAlaIleGlyValProGluProLysSerValPheValAsp 321  
QY 1040 ACCTATGGCAGCGGAGATCCATGATAGGAGATTCATCAATGCTGAGGAGACTTT 1099  
Db 322 SerTyrGlyThrGlyGlnIleProAspLysGluIleLeuAsnIleValLysGluAsnPhe 341  
QY 1100 GATTTCCAGGCGCGTATGATCTCCATCAACCTTGTATCTCAAGAGGGTGGGATACAGG 1159  
Db 342 AspPheArgProGlyMetIleThrIleAsnLeuAspLeuLysArgGlyGlyAsnGlyArg 361  
QY 1160 TTCTTGAAGACTGCTGCATATGACACTTCGGCAGAGAGGACCCCTGACTTCATGGGAA 1219  
Db 362 PheLeuLysThrAlaGlyTyrGlyHisPheGlyArgAspAspProAspPheThrTrpGlu 381  
QY 1220 GTGGTCAAGCCCTCAAGTGGGAGAG 1246  
Db 382 IleValLysProLeuLysTrpGluLys 390

RESULT 7  
METK\_POPDE STANDARD; PRT; 395 AA.  
ID METK\_POPDE  
AC P479T6;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE S-adenosylmethionine synthetase (EC 2.5.1.6) (Methionine  
adenosyltransferase) (AdoMet synthetase).  
OS Populus deltoides (Poplar).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
OC eurosid I; Malpighiales; Salicaceae; Populus.  
OX NCBI\_TaxID:3696;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE:Leaf;  
RX MEDLINE=94105359; PubMed=8278561; DOI=10.1104/pp.102.4.1365;  
RA van Doorselaere J., Gielen J., van Montagu M., Inze D.;  
RT "A cDNA encoding S-adenosyl-L-methionine synthetase from poplar.";  
RL Plant Physiol. 102:1365-1366(1993).  
CC -!- FUNCTION: Catalyzes the formation of S-adenosylmethionine from  
methionine and ATP.  
CC -!- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +  
diphosphate + S-adenosyl-L-methionine.  
CC -!- COFACTOR: Binds 2 divalent ions, such as magnesium or cobalt, and  
1 potassium ion per subunit (By similarity).  
CC -!- PATHWAY: Activated methyl cycle.  
CC -!- SIMILARITY: Belongs to the AdoMet synthetase family.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See http://www.isb-sib.ch/announce/  
or send an email to license@sib-sib.ch).  
CC EMBL; M73430; AAA20112.1; --  
DR HSP; P13444; 1QW4.  
DR InterPro; IPR002133; S-AdoMet\_synt.  
DR Pfam; PF02773; S-AdoMet\_synt\_C; 1.  
DR Pfam; PF02772; S-AdoMet\_synt\_M; 1.  
DR Pfam; PF00438; S-AdoMet\_synt\_N; 1.  
DR PIRSF; PIRSF000497; MAT; 1.  
DR TIGRPFAMs; TIGR01034; metK; 1.  
DR PROSITE; PS00376; ADOMET SYNTHETASE\_1; 1.  
DR PROSITE; PS00377; ADOMET SYNTHETASE\_2; 1.  
KW ATP-binding; Magnesium; Metal-binding; Multigene family;  
KW One-carbon metabolism; Potassium; Transferase.  
FT NP\_BIND 120 125 ATP (Potential).  
FT METAL 18 18 Magnesium (By similarity).  
FT METAL 44 44 Potassium (By similarity).  
FT METAL 272 272 Potassium (By similarity).  
FT METAL 280 280 Magnesium (By similarity).  
FT BINDING 148 148 ATP (Potential).  
SQ SEQUENCE 395 AA; 43269 MW; 6E90404CE1CD0FCC CRC64;  
Alignment Scores:  
Pred. No.: 8,23e-146 Length: 395  
Score: 1989.00 Matches: 373  
Percent Similarity: 97.95% Conservative: 9  
Best Local Similarity: 95.64% Mismatches: 8  
Query Match: 72.38% Indels: 0  
DB: 1 Gaps: 0  
US-10-734-698A-38 (1-1485) x METK\_POPDE (1-395)

QY 74 ATGGCAGAGACATTCCTATTACCTCAGAGTCAGTGACGGGACACCTGACAGCTC 133  
Db 1 MetAlaGluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeu 20



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QY 134 TGCACCAAAATCTCGATGCTGCTCGACGCTTGCCTTGAACAGAGACCACGACGACGAG 193
Db 21 CysAspGlnIleSerAspAlaValLeuAspAlaCysLeuAlaGlnAspProAspSerLys 40
QY 194 GTTGCTCGCAAAATGACCAAGACCAACTTGGTCATGGTCTTCGAGAGATCAACCACC 253
Db 41 ValAlaCysGluThrCysThrLysThrAsnMetValMetValPheGlyGluIleThrThr 60
QY 254 AGGCCAACGTTGACTACAGAGATCGTGCCTGACACCTGAGAAACATCGGCTTCGTC 313
Db 61 LysAlaAspValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheThr 80
QY 314 TCAACAGATGCGGACTTCATGCTGACAACTGCAAGTCTTGTAAACATTCAGAGAGAG 373
Db 81 SerAlaAspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGln 100
QY 374 AGCCCTGATATTGCCAGGTTGACACGGCCACCTTACCAAAAGACCCGAGGAATTCGGT 433
Db 101 SerProAspIleAlaGlnGlyValHisGlyHisPheSerLysArgProGluGluIleGly 120
QY 434 GCTGGAGACAGGTCACATGTTGGCTATGTCACAGGAGAAACCCAGAAATTCATGACCA 493
Db 121 AlaGlyAspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetPro 140
QY 494 TTGAGTCATGTTCTGCAACTAACTCGGTGCTCGCTCACCGAGGTTGCGCAAGAACGGA 553
Db 141 LeuSerHisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGly 160
QY 554 ACCTGCCCATGTTGAGGCTGATGGGAAACCAAGTGACTGTTGAGTATTACATGAC 613
Db 161 ThrCysAlaTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnGlu 180
QY 614 ACGGTGCCATGTTCCAGTTCGTGTCACACTGCTTATCTCCACCAACATGATGAG 673
Db 181 AsnGlyAlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGlu 200
QY 674 ACTGTCAACCAACGACAAATTCGACGTGACCTCAAGGAGCATGTGATCAAGCGGTGATC 733
Db 201 ThrValThrAsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIle 220
QY 734 CCGGAGAAGTACTTGATGAGAGACCAATTTTCCACTTGAACCCCTTCGGCGGTTTGTGC 793
Db 221 ProGluLysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheVal 240
QY 794 ATTGAGGTCCTCACGGTCATGCTGCTCACGGCCGCAAGATCATCATCATCTTAC 853
Db 241 IleGlyGlyProHisGlySerGlyLeuThrGlyArgLysIleIleIleAspThrTyr 260
QY 854 GGAGGATGGGTGCTCATGCTGCTGCTGCTTCTCCGGGAAGGATCCCAACCAAGTGTGAT 913
Db 261 GlyGlyTyrGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAsp 280
QY 914 AGGAGTGTGCTTACATTTGTGACAGAGGCTGCTTAAGAGCATTTGTGGCAAGTGAGTCC 973
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QY 974 AGAAGTGTGATGTGCAAGTCTTATGCTGCTGCTGCTGCTCCCGAGGCTTGTCTGCTTT 1033
Db 301 ArgArgCysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPhe 320
QY 1034 GTTGACACCTATGGCACCGGGAAGATCCATGATAGGAGATCTCAACATTCGTAAGGAG 1093
Db 321 ValAspThrTyrGlyThrGlyLysIleProAspLysGluIleGlnIleValLysGlu 340
QY 1094 AACTTTGATTTAGGCCCGGTTGATCTCCATCAACTTGTATCTCAAGAGGGGTGGGAAT 1153
Db 341 ArgPheAspPheArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyGlyAsn 360
QY 1154 AACAGTTCCTGAAGACTCTGATATGACACTTCGGCAGAGAGACCCCTCACTTACA 1213
Db 361 SerArgPheLeuLysThrAlaAlaTyrGlyHisPheGlyArgAspProAspPheThr 380
QY 1214 TGGGAAGTGTGTCAGGCCCTCAAGTGGGAG 1243
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Db 381 TrpGluValValLysProLeuLysTrpAsp 390
RESULT 8
Q84MM2 PRELIMINARY; PRT; 393 AA.
AC Q84MM2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE S-adenosylmethionine synthetase.
OS Name=SAMS;
GN Litchi chinensis.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Sapindales; Sapindaceae; Litchi.
OX NCBI_TaxID=151069;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y.-S., Xu X., Huang S.-Z., Fu J.-R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Catalyzes the formation of S-adenosylmethionine from
methionine and ATP (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
diphosphate + S-adenosyl-L-methionine.
CC -!- COFACTOR: Binds 2 divalent ions, such as magnesium or cobalt, and
1 potassium ion per subunit (By similarity).
CC -!- PATHWAY: Activated methyl cycle.
CC -!- SIMILARITY: Belongs to the AdoMet synthetase family.
DR EMBL; AY259227; AAP13994.1; -.
DR HSP; P13444; 10M4.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0000287; P:magnesium ion binding; IEA.
DR GO; GO:0004478; F:methionine adenosyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006730; P:one-carbon compound metabolism; IEA.
DR InterPro; IPR002133; S-AdoMet synt.
DR Pfam; PF02772; S-AdoMet synt_M; 1.
DR Pfam; PF00438; S-AdoMet synt_N; 1.
DR PIRSF; PIRSF000497; MAT; 1.
DR TIGRFAMs; TIGR01034; metK; 1.
DR PROSITE; PS00376; ADOMET SYNTHETASE 1; 1.
DR PROSITE; PS00377; ADOMET SYNTHETASE 2; 1.
KW ATP-binding; Magnesium; Metal-binding; One-carbon metabolism;
KW Potassium; Transferase
SQ SEQUENCE 393 AA; 42504 MW; CCB5423C334BEC3 CRC64;
Alignment Scores:
Pred. No.: 1,41e-145 Length: 393
Score: 1986.00 Matches: 370
Percent Similarity: 98.20% Conservative: 12
Best Local Similarity: 95.12% Mismatches: 7
Query Match: 72.27% Indels: 0
DB: 2 Gaps: 0
US-10-734-698A-38 (1-1485) x Q84MM2 (1-393)
QY 80 GAGACATTCCTATTACCTCAGAGTCAGTGAACGAGGAGACCCCTGACCAAGCTCTGCGAC 139
Db 2 GluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCysAsp 21
QY 140 CAATCTCCGATGCTGCTCGACGCTTGCCTTGAACAGGACCCAGACAGCAAGGTTGCC 199
Db 22 GlnValSerAspAlaValLeuAspAlaCysLeuAlaGlnAspProAspSerLysValAla 41
QY 200 TCGAAACATGCACCAAGACCAACTTGGTCATGCTTCGAGAGATCACCACCAAGGCC 259
Db 42 CysGluThrCysThrArgThrAsnMetValMetValPheGlyGluIleThrThrLysAla 61
QY 260 AACGTTGACTACGAGAGATCGTGGTCACACCTGCGAGGAACATCGGCTTCGCTCAAC 319
Db 62 AsnValAspTyrGluGlnIleValArgAspThrCysArgSerIleGlyPheThrSerAsp 81
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QY 320 GATGTGGGCTTGTATGCTGACAACTGCAAGGTCTCTGTAAACATTTGAGCAGCAGCCCT 379  
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 QY 380 GATATTGCCAGGCTGTGACGCGCCACTTACCAGAGACCCGAGGAAATCGGTGCTGGA 439  
 Db 102 AspIleAlaGlnGlyValHisGlyHisLeuThrLysLysProGluGluLeuGlyAlaGly 121  
 QY 440 GACCAGGCTCACATGTTGGCTATGCCAGCAGCAAAACCCAGAAATTTGATGCTATGAGT 499  
 Db 122 AspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuSer 141  
 QY 500 CATGTTCTTGCACATAAATCGGTGCTGCTCACCAGAGTTGCGAAGAACGAACTGCG 559  
 Db 142 HisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThrCys 161  
 QY 560 CCATGTTGAGGCTCATGTTGAGAAACCCCAAGTCACTGTTGAGTATTACATGACACGGT 619  
 Db 162 AlaTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnGlyAsnGly 181  
 QY 620 GCCATGTTCCAGTTCGTGTCACACTGTGCTTATCTCCACCAACATGATGAGACTGTG 679  
 Db 182 AlaMetValProValArgValHisThrValLeuLeuSerThrGlnHisAspGluThrVal 201  
 QY 680 ACCAAGCAGAAATTCAGCTGACCTCAAGGACGATGATCAAGCCGGTGATCCCGAG 739  
 Db 202 ThrAsnAspGluIleAlaAlaAspLeuLysGlnHisValIleLysProValIleProGlu 221  
 QY 740 AAGTACCTTGATGAGAGACCAATTTCCACTTGAACCCCTGCGCGTTTTCATTCGGA 799  
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 QY 800 GGTCTCTCAGCGTGATGCTGCTCCTCAGCGCGCAGACATCATCATCATCTTACGGAGA 859  
 Db 242 GlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyrGlyGly 261  
 QY 860 TGGGGTCTCATGTTGGTGGTCTTTCTCGGGAAGGATCCCAAGAGTTGATAGAGT 919  
 Db 262 TrpGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSer 281  
 QY 920 GGTGCTTACATGTGAGACAGCTGCTAGACATTTGCGAGCTTGTGCTGCTTGTGAC 979  
 Db 282 GlyAlaTyrIleValArgGlnAlaAlaLysSerIleValAlaSerGlyLeuAlaArg 301  
 QY 980 TGCAATGTGCAAGTGTCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1039  
 Db 302 CysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAsp 321  
 QY 1040 ACTATGCGACCGGGAAGATCCATGATAAGGAGTCTCAACATTTGTAAGGAGAACTTT 1099  
 Db 322 SerTyrGlyThrGlyLysIleProAspArgGluIleLeuLysIleValLysGluAsnPhe 341  
 QY 1100 GATTTCCAGCGCGGTATGATCTCCATCACTTGTATCAAGGGGTGGGATACAGG 1159  
 Db 342 AspPheArgProGlyMetIleSerValAsnLeuAspLeuLysArgGlyGlyAsnGlyArg 361  
 QY 1160 TTCTTGAACACTGCTCATATGACACTTTCGCGCAGAGAGCCCTGACTTTCATCGGAA 1219  
 Db 362 PheLeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThrTrpGlu 381  
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 Db 382 ValValLysProLeuLysTrpAspLys 390  
 RESULT 9  
 METK\_LYCES  
 ID METK\_LYCES STANDARD; PRT; 393 AA.  
 AC P43280;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE S-adenosylmethionine synthetase 1 (EC 2.5.1.6) (Methionine  
 adenosyltransferase 1) (AdoMet synthetase 1).

GN Name=SAM1;  
 OS Lycopersicon esculentum (Tomato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC lamids; Solanales; Solanaceae; Solanum.  
 OX NCBI\_TaxID=4081;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Rutgers;  
 RX MEDLINE=9428946; PubMed=8018871;  
 RA Espartaco J., Pintor-Toro J.A., Pardo J.M.;  
 RT "Differential accumulation of S-adenosylmethionine synthetase  
 transcripts in response to salt stress.";  
 RL Plant Mol. Biol. 25:217-227(1994).  
 CC -!- FUNCTION: Catalyzes the formation of S-adenosylmethionine from  
 CC methionine and ATP.  
 CC -!- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +  
 CC diphosphate + S-adenosyl-L-methionine.  
 CC -!- COFACTOR: Binds 2 divalent ions, such as magnesium or cobalt, and  
 CC 1 potassium ion per subunit (By similarity).  
 CC -!- PATHWAY: Activated methyl cycle.  
 CC -!- SIMILARITY: Belongs to the AdoMet synthetase family.  
 CC  
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 CC or send an email to license@isb-sib.ch).  
 CC  
 CC EMBL; Z24741; CAA80865.1; -;  
 DR PIR; S46538; S46538.  
 DR HSP; P13444; 10M4.  
 DR InterPro; IPR002133; S-AdoMet\_synt.  
 DR Pfam; PF02773; S-AdoMet\_synt\_C; 1.  
 DR Pfam; PF02772; S-AdoMet\_synt\_M; 1.  
 DR Pfam; PF00438; S-AdoMet\_synt\_N; 1.  
 DR PIRSF; PIRSF000497; MAT; 1.  
 DR TIGRFAMs; TIGR01034; metK; 1.  
 DR PROSITE; PS00376; ADOLET\_SYNTHETASE\_1; 1.  
 DR PROSITE; PS00377; ADOLET\_SYNTHETASE\_2; 1.  
 KW ATP-binding; Magnesium; Metal-binding; Multigene family;  
 KW One-carbon metabolism; Potassium; Transferase.  
 FT NP\_BIND 119 124 ATP (Potential).  
 FT METAL 17 17 Magnesium (By similarity).  
 FT METAL 43 43 Potassium (By similarity).  
 FT METAL 271 271 Potassium (By similarity).  
 FT METAL 279 279 Magnesium (By similarity).  
 FT BINDING 147 147 ATP (Potential).  
 SQ SEQUENCE 393 AA; 43301 MW; 81433A565A68039B CRC64;  
 Alignment Scores:  
 Pred. No.: 1.68e-145 Length: 393  
 Score: 1985.00 Matches: 374  
 Percent Similarity: 97.69% Conservatve: 6  
 Best Local Similarity: 96.14% Mismatches: 9  
 Query Match: 72.23% Indels: 0  
 Db: 1 Gaps: 0  
 US-10-734-698A-38 (1-1485) x METK\_LYCES (1-393)  
 QY 80 GAGACATTCTCTATTACCTCAGAGTCAGTGAACGAGGACACCTTGACAGCTCTGCGAC 139  
 Db 2 GluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCysAsp 21  
 QY 140 CAAATCTCCGATGCTGCTCTCGACGCTTGCCTTGAACAGGACCCACAGCAGAGTTGCC 199  
 Db 22 GlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProGluSerLysValAla 41  
 QY 200 TCGGAACATCGACCAAGACCACTTGCTGCTATGCTTCTCGGAGAGATCACCACCGGCC 259  
 Db 42 CysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThrTyrSala 61

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QY 260 AACGTTGACTACGAGAAGATCGTGGTGACCTGCAGGAACATCGGCTTCCTCCAAAC 319
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QY 62 IlevAlAspIyGluLysIleValArgAspThrCysArgAsnIleGlyPheValSerAsp 81
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QY 320 GATGTGGGACTTGATGCTGACAACTGCAAGTCCCTTTGTAACATTCAGCAGCAGCCCT 379
Db |||
QY 82 AspValGlyLeuAspAlaAspAsnCysLysValLeuValTyrIleGluGlnGlnSerPro 101
Db |||
QY 380 GATATTGCCAGGGTGTGCAGGCCACCTTACAAAGAACCCGAGAGAAATCGGTCTGGA 439
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QY 102 AspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGlyAlaGly 121
Db |||
QY 440 GACCAAGGTCACATGTTTCGCTATGCCAGCGACGAAACCCAGAAATTCATGATCGATGAGT 499
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QY 122 AspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuSer 141
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QY 500 CATGTTCTTGGCAACTAAATCTCGGTGCTGCTCACCAGAGTTCGCAAGAACCGAACTGCC 559
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QY 142 HisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThrCys 161
Db |||
QY 560 CCATGTTGAGGCTGATCGGAAAAACCCAAAGTGACTGTTGAGTATTACAAATGACACCGGT 619
Db |||
QY 162 AlaTrpLeuArgProAspGlyLysThrGlnValThrValGluTyr-SerAsnAspAsnGly 181
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QY 620 GCATGTTTCCAGTTCGTCACACTGCTGCTTATCTCCACCAACATGATGAGACTGTG 679
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QY 182 AlaMetValProIleArgValHisThrValLeuIleSerThrGlnHisAspGluThrVal 201
Db |||
QY 680 ACCAAGCAGCAATTCGAGTGCACCTCAAGGAGCATGTGATCAAGCCGGTGTATCCCGGAG 739
Db |||
QY 202 ThrAsnAspGluIleAlaArgAspLeuLysGluHisValIleLysProValIleProGlu 221
Db |||
QY 740 AGTACTCTTGAGAGAAACCATTTTCCACTTGTAACCCCTCTGCGCGTTTGTTCATTTGA 799
Db |||
QY 222 LysTyrLeuAspGluAsnThrIlePheHisLeuAsnProSerGlyArgPheValIleGly 241
Db |||
QY 800 GGTCTCTCAGGTGATGCTGCTCTCACCAGCCGACAGATCATCATGATCATTCACGAGGA 859
Db |||
QY 242 GlyProHisGlyAspAlaGlyLeuThrGlyArgGlyIleIleAspThrTyrGlyGly 261
Db |||
QY 860 TGGGTGCTCATGTTGGTGGTGTCTTCTCCGGGAAGGATCCCAACCAAGGTTGATAGGAGT 919
Db |||
QY 262 TrpGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSer 281
Db |||
QY 920 GGTGCTTACATTTGTGAGACAGCTGCTAAGACATTTGTGGCAAGTGGACTACCGAAGG 979
Db |||
QY 282 GlyAlaTyrIleValArgGlnAlaAlaLysSerIleValAlaSerGlyLeuAlaArg 301
Db |||
QY 980 TGCATTGTCAAGTGTCTTATGCCATTGCTGCTGTCGCGAGCCCTTCTGCTCTTGTTCAC 1039
Db |||
QY 302 CysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAsp 321
Db |||
QY 1040 ACCTATGGCACCGGGAAGATTCATGATAAGGAGATTCCTCAACATTTGTGAAGGAGAACTTT 1099
Db |||
QY 322 ThrTyrGlyThrGlyLysIleProAspArgGluIleLeuLysIleValLysGluAsnPhe 341
Db |||
QY 1100 GATTTCAAGCCCGGTATGATTCATCAACCTTGTATCTCAAGAGGGGTGGGAATACACAG 1159
Db |||
QY 342 AspPheArgProGlyMetMetSerIleAsnLeuAspLeuLysArgGlyGlyAsnArgArg 361
Db |||
QY 1160 TTCTTCAAGACTGCTGCATATGGACACTTTCGCGAGAGAGCCCTGACTTCATCGGGA 1219
Db |||
QY 362 PheLeuLysThrAlaAlaTyrGlyHisPheGlyArgAspProAspPheThrTrpGlu 381
Db |||
QY 1220 GTGGTCAAGCCCTCAAGTGGGAGAG 1246
Db |||
QY 382 ValValLysProLeuLysTrpGluLys 390
Db |||
RESULT 10
METL_LYCES
ID METL_LYCES STANDARD; PRT; 393 AA.
AC P43281;
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DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE S-adenosylmethionine synthetase 2 (EC 2.5.1.6) (Methionine
DE adenosyltransferase 2) (AdoMet synthetase 2).
GN Name=SAM2;
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Rutgers;
RX MEDLINE=94289646; PubMed=8018871;
RA Espartaco J., Pintor-Toro J.A., Pardo J.M.;
RT "Differential accumulation of S-adenosylmethionine synthetase
RT transcripts in response to salt stress.";
RL Plant Mol. Biol. 25:217-227(1994).
CC -!- FUNCTION: Catalyzes the formation of S-adenosylmethionine from
CC methionine and ATP.
CC -!- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
CC di-phosphate + S-adenosyl-L-methionine.
CC -!- COFACTOR: Binds 2 divalent ions, such as magnesium or cobalt, and
CC 1 potassium ion per subunit (By similarity).
CC -!- PATHWAY: Activated methyl cycle.
CC -!- SIMILARITY: Belongs to the AdoMet synthetase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z24742; CAA80866.1; -.
DR PIR; S46539; S38875.
DR HSP; P13444; IQM4.
DR InterPro; IPR002133; S-AdoMet_synt.
DR Pfam; PF02773; S-AdoMet_synt_C; 1.
DR Pfam; PF02772; S-AdoMet_synt_M; 1.
DR Pfam; PF00438; S-AdoMet_synt_N; 1.
DR PIRSF; PIRSF00497; MAT; 1.
DR TIGRFAMs; TIGR01034; metK; 1.
DR PROSITE; PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE; PS00377; ADOMET_SYNTHETASE_2; 1.
DR ATP-binding; Magnesium; Metal-binding; Multigene family;
KW One-carbon metabolism; Potassium; Transferase.
FT NP_BIND 119 124 ATP (Potential).
FT METAL 17 17 Magnesium (By similarity).
FT METAL 43 43 Potassium (By similarity).
FT METAL 271 271 Potassium (By similarity).
FT METAL 279 279 Magnesium (By similarity).
FT BINDING 147 147 ATP (Potential).
SQ SEQUENCE 393 AA; 43081 MW; 4877D0D1B21BFD79 CRC64;

Alignment Scores:
Pred. No.: 2,41e-145 Length: 393
Score: 1983.00 Matches: 371
Percent Similarity: 97.69% Conservative: 9
Best Local Similarity: 95.37% Mismatches: 9
Query Match: 72.16% Indels: 0
DB: 1 Gaps: 0

US-10-734-698A-38 (1-1485) x METL_LYCES (1-393)
QY 80 GAGACATTCTTATTACCTCAGAGTCAGTGAACGAGGACACCTTGACAGCTCTGCAC 139
Db |||
Db 2 GluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCysAsp 21
QY 140 CAATCTCCGATGCTGCTCTCGACGCTTGTGCTTGAACAGGACCCACAGCAAGGTTCGC 199
|||:::|||||
|||:::|||||
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Db 22 GlnValSerAspAlaValLeuAspAlaCysLeuAlaGlnAspProGluSerLysValAla 41  
QY 200 TCGAAACATGCACCAAGACCAACTTGGTCATGCTCTTCGGAGAGATCACCAACCAAGGCC 259  
Db 42 CysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThrLysAla 61  
QY 260 AAGTTGATACAGAAAGATCGTCGTGACACCTGCAGGAACATCGGCTTGTCTCAAC 319  
Db 62 AsnIleAspTyrGluLysIleValArgAspThrCysArgGluIleGlyPheValSerPro 81  
QY 320 GATGTGGAGCTTCATGCTGCAACTGCAAGTCTCTGTAAACATTCAGCAGCAGACCCCT 379  
Db 82 AspValGlyLeuAspAlaAspCysArgValLeuValAsnIleGluGlnGlnSerPro 101  
QY 380 GATATTGCCAGGGTGTGACGGCCACCTTACCAAAAGACCCGAGGAATTCGGTGTGGA 439  
Db 102 AspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGlyAlaGly 121  
QY 440 GACCAGGTCACATGTTGGCTATGCCAGGAGCAACCCAGAAATGATGCCATGAGT 499  
Db 122 AspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuSer 141  
QY 500 CATGTTCTTCCAACTAACTCGTGTCTGCTCACCGAGGTTCCGAGAACCGAACCTGC 559  
Db 142 HisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThrCys 161  
QY 560 CATGTTGAGGCTCATGCGAAACCAAGTGAAGTGAATTCATCAATCAACACGGT 619  
Db 162 SerTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrHisAsnAspAsnGly 181  
QY 620 GCATGGTTCATGCTGTCACACTGTGCTTATCTCCACCAACCAATGATGAGACTGTG 679  
Db 182 AlaMetValProLeuArgValHisThrValLeuIleSerThrGlnHisAspGluThrVal 201  
QY 680 ACCAAGCAGAAATTCAGCTGACCTCAAGGACATGTGATCAAGCGGTGATCCCGGAG 739  
Db 202 ThrAsnAspGluIleAlaArgAspLeuLysGluHisValIleLysProValIleProGlu 221  
QY 740 AAGTACTTGATGAGAGACCATTTTCCACTTCAACCCCTCTGGCGTGTGTTCATGTGA 799  
Db 222 LysTyrLeuAspGluAsnThrIlePheHisLeuAsnProSerGlyArgPheValIleGly 241  
QY 800 GGTCTCTCAGCTGATGCTGCTCTCACCGCGCAAGATCATCATCATCATCATCATCAT 859  
Db 242 GlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleIleAspThrTyrGlyGly 261  
QY 860 TGGGTGCTCATGCTGCTGCTTCTCGGGAAGGATCCCAAGCTTGTATAGGACT 919  
Db 262 TrpGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSer 281  
QY 920 GGTGCTTACATTTGAGACAGGCTGCTTAAGACATTTGTGGCAAGTGGACTAGCAGAGG 979  
Db 282 GlyAlaTyrIleValArgGlnAlaAlaLysSerIleValAlaAsnGlyLeuAlaArg 301  
QY 980 TGCAATGTGCAAGTGTCTTATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1039  
Db 302 CysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAsp 321  
QY 1040 ACCTATGGCAGCGGAGATCCATGATAGGAGATTCATCAACTTGTGAAGGACTTT 1099  
Db 322 ThrTyrGlyThrGlyLysIleProAspLysGluIleLeuAsnIleValLysGluAsnPhe 341  
QY 1100 GATTTCCAGGCGCGGTATGATCTCCATCAACTTGTATCTCAAGAGGGTGGGATACAGG 1159  
Db 342 AspPheArgProGlyMetIleSerIleAsnLeuAspLeuArgGlyLysAsnGlyArg 361  
QY 1160 TTCTTGAAGACTGCTCATATGACACTTCGGCAGAGAGACCTCATCTCATCTCATCTG 1219  
Db 362 PheLeuLysThrAlaAlaTyrGlyHisPheGlyArgAspAspPheThrTrpGlu 381  
QY 1220 GTGGTCAAGCCCTCAAGTGGGAGAG 1246  
Db 382 ValValLysProLeuLysTrpAspLys 390

## RESULT 11

Q9SBQ7 PRELIMINARY; PRT; 393 AA.  
ID Q9SBQ7, AC Q9SBQ7, DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAY-2004 (TREMBLrel. 26, Last annotation update)  
DE S-adenosyl-L-methionine synthetase.  
OS Petunia hybrida (Petunia).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC Lamiales; Solanales; Solanaceae; Petunia.  
NCBI\_TaxID=4102;  
RN [1]  
RX SEQUENCE FROM N.A.  
RC TISSUE=Corolla;  
RX MEDLINE=20027448; PubMed=10557255;  
RA Soong S.C., To K.Y.;  
RT "Nucleotide Sequence Of A cDNA (AF170798) Encoding Type I S-Adenosyl-  
L-Methionine Synthetase From Petunia hybrida. (PGR99-160).";  
RL Plant Physiol. 121:1053-1053(1999).  
CC -I- FUNCTION: Catalyzes the formation of S-adenosylmethionine from  
methionine and ATP (By similarity).  
CC -I- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +  
diphosphate + S-adenosyl-L-methionine.  
CC -I- COFACTOR: Binds 2 divalent ions, such as magnesium or cobalt, and  
1 potassium ion per subunit (By similarity).  
CC -I- PATHWAY: Activated methyl cycle.  
CC -I- SIMILARITY: Belongs to the AdoMet synthetase family.  
EMBL; AF170798; AAC48485.1; -.  
DR HSSP; P13444; 1QM4.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:000287; F:magnesium ion binding; IEA.  
DR GO; GO:0004478; F:methionine adenosyltransferase activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0006730; P:one-carbon compound metabolism; IEA.  
DR InterPro; IPR002133; S-AdoMet\_synth.  
DR Pfam; PF02773; S-AdoMet\_synth\_G; 1.  
DR Pfam; PF02772; S-AdoMet\_synth\_M; 1.  
DR Pfam; PF00438; S-AdoMet\_synth\_N; 1.  
DR FIRSF; FIRSF000497; NAT; 1.  
DR TIGRFAMs; TIGR01034; metK; 1.  
DR PROSITE; PS00376; ADOMET SYNTHETASE 1; 1.  
DR PROSITE; PS00377; ADOMET SYNTHETASE 2; 1.  
KW ATP-binding; Magnesium; Metal-binding; One-carbon metabolism;  
KW Potassium; Transferase.  
SQ SEQUENCE 393 AA; 43169 MW; 0ACDD62F28F6749 CRC64;  
Alignment Scores:  
Pred. No.: 4,92e-145 Length: 393  
Score: 1979.00 Matches: 372  
Percent Similarity: 97.6% Conservatives: 9  
Best Local Similarity: 95.3% Mismatches: 9  
Query Match: 72.0% Indels: 0  
DB: 2 Gaps: 0  
US-10-734-698A-38 (1-1485) x Q9SBQ7 (1-393)

QY 80 GAGACATTCCTATTATTACCTCAGAGTCAAGAGGAGACACCTGACAGGCTCTCGGAC 139  
Db 2 GluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCysAsp 21  
QY 140 CAAATCTCCGATGCTGCTCGACGCTTGCCTTGAACAGAGCCAGACAGAGGTTGCC 199  
Db 22 GlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProGluSerLysValAla 41  
QY 200 TCGCAAAACATGCACCAAGACCAACTTGGTTCATGGTCTTCGGAGAGATCACCAAGGCC 259  
Db 42 CysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThrLysAla 61  
QY 260 AACGTTGATACGAGAGATCGTGGTGACACCTGAGGAAACATCGGCTTCCTCAAC 319  
Db 260 AACGTTGATACGAGAGATCGTGGTGACACCTGAGGAAACATCGGCTTCCTCAAC 319

Db 62 AsnValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheIleSerAsp 81  
Qy 320 GATGTGGGACTTGATGCTGACAACTGCAGAGTCCCTGTAAACATTTGACGACGAGCCCT 379  
Db 82 AspValGlyLeuAspAlaAspAsnCysIleValLeuValTyrIleGluGlnSerPro 101  
Qy 380 GATATTGCCCGGCTGTGACCGCCACCTTACCAAAAGACCCGAGGAATCGGTCTGA 439  
Db 102 AspIleAlaGlnGlyValHisGlyHisLeuThrLysGlnProGluGluIleGlyAlaGly 121  
Qy 440 GACCAAGGTCACATGTTTCGCTATGCCACGACGAGAAACCCAGAAATTTGATGCAATGAGT 499  
Db 122 AspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluPheMetProLeuSer 141  
Qy 500 CATGTTCTTGCAACTAACTCGTCTGCTCTCACCAGGTTTCGCAAGACCGAACCTTGC 559  
Db 142 HisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThrCys 161  
Qy 560 CCATGTTGAGCGCTGATGGGAAACCCCAAGTGACTGTTGAGTATTACAAATGACACGCT 619  
Db 162 ProTrpLeuArgProAspGlyThrGlnValThrValGluTyrTyrAsnGluAsnGly 181  
Qy 620 GCATGTTCCAGTTCGTGTCACACTGTGCTTATCTCCACCCCAACATGATGAGACTGTG 679  
Db 182 AlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGluThrVal 201  
Qy 680 ACCAAGGACAAATTGCACCTGACCTCAGGAGCATGTGATCAAGCCGTGATCCGGAG 739  
Db 202 ThrAsnAspGluIleAlaHisAspLeuLysGluHisValIleLysProValIleProGlu 221  
Qy 740 AAGTACTCTTGATGAGAAGACCATTTTCCACTTGTAACCCCTCTGGCGCTTTGTCATTGA 799  
Db 222 LysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheValIleGly 241  
Qy 800 GGTCTCTACGCTGATGCTGCTCTCACCAGCCGCAAGATCATCATCATCTTACGAGGA 859  
Db 242 GlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyrGlyGly 261  
Qy 860 TGGGGTGTCTATGGTGGTGGTCTTCTCCGGGAGGATCCCAACCAAGTTGATAGGAGT 919  
Db 262 TrpGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSer 281  
Qy 920 GGTGCTTACATTTGTGAGACAGCGCTGCTAAGAGCATTTGTGGCAAGTGGACTAGCCAGAAGG 979  
Db 282 GlyAlaTyrIleValArgGlnAlaLysSerValValAlaAsnGlyLeuAlaArg 301  
Qy 980 TGCATTGTCCAAGTGTCTATGCCATTGTGTCGCCGAGCCCTTTGTCTCTTTGTGAC 1039  
Db 302 CysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAsp 321  
Qy 1040 ACCTATGGCACCGGAGAGATCCATGATAAGGAGATCTCAACATTTGTGAGGAGAACTTT 1099  
Db 322 ThrTyrGlyThrGlyMetIleProAspLysGluIleLeuLysIleValLysGluAsnPhe 341  
Qy 1100 GATTTCCAGCCCGGTATGATCTCATCAACCTTGATCTCAAGAGGGTGGGAATAACAGG 1159  
Db 342 AspPheArgProGlyMetIleAlaIleAsnLeuAspLeuLysArgGlyAsnGlyArg 361  
Qy 1160 TTCTTGAAGACTGCTGATATGACACTTCGGCAGAGAGGACCTGACTTCAATGGGAA 1219  
Db 362 PheLeuLysThrAlaAlaTyrGlyHisPheGlyArgAspAspThrAspPheThrTrpGlu 381  
Qy 1220 GTGGTCAAGCCCTCAAGTGGGAGAGGCC 1249  
Db 382 ValValLysProLeuLysCysGluLysAla 391

## RESULT 12

Q944U4 PRELIMINARY; PRT; 395 AA.  
AC Q944U4; (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 26, Last annotation update)

DE S-adenosyl-L-methionine synthetase.  
GN Name=Same;  
OS Dendrobium crumenatum (Tropical pigeon orchid)  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;  
OC Epidendroideae; higher Epidendroideae; Dendrobieae; Dendrobieae;  
OC Dendrobium.  
OX NCBI\_TaxID=51096;  
RN [1]\_TaxID=51096;  
RP SEQUENCE FROM N.A.  
RA Han P., Pua E.C.;  
RL Submitted (Sep-2001) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Catalyzes the formation of S-adenosylmethionine from  
CC methionine and ATP (By similarity).  
CC -!- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +  
CC diphosphate + S-adenosyl-L-methionine.  
CC -!- COPACITOR: Binds 2 divalent ions, such as magnesium or cobalt, and  
CC 1 potassium ion per subunit (By similarity).  
CC -!- PATHWAY: Activated methyl cycle.  
CC -!- SIMILARITY: Belongs to the AdoMet synthetase family.  
DR EMBL; AF420238; AAL16064.1; -.  
DR HSPF; P13444; IQM4.  
DR GO; GO:0005524; P:ATP binding; IEA.  
DR GO; GO:0000287; F:magnesium ion binding; IEA.  
DR GO; GO:0004478; F:methionine adenosyltransferase activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0006730; P:one-carbon compound metabolism; IEA.  
DR InterPro; IPR002133; S-AdoMet\_synth.  
DR Pfam; PF02772; S-AdoMet\_synth\_C; 1.  
DR Pfam; PF02773; S-AdoMet\_synth\_N; 1.  
DR PIRSF; PIRSF00497; MAT; 1.  
DR TIGRFAMs; TIGR01034; metK; 1.  
DR PROSITE; PS00376; ADOMET\_SYNTHETASE\_1; 1.  
DR PROSITE; PS00377; ADOMET\_SYNTHETASE\_2; 1.  
KW ATP-binding; Magnesium; Metal-binding; One-carbon metabolism;  
KW Potassium; Transferase.  
SQ SEQUENCE 395 AA; 43210 MW; 240AAA4A7CF8DA440 CRC64;

## Alignment Scores:

Pred. No.: 1,1e-144 Length: 395  
Score: 1974.50 Matches: 370  
Percent Similarity: 97.71% Conservative: 14  
Best Local Similarity: 94.15% Mismatches: 6  
Query Match: 71.85% Indels: 3  
Gaps: 2

US-10-734-698A-38 (1-1485) x Q944U4 (1-395)

Qy 74 ATGGCAGAG-----ACATTCTATTACCTCAGAGTCAGTGAACGAGGACACCCCTGAC 127  
Db 1 MetAlaGluValAspThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAsp 20  
Qy 128 AAGCTCTGCGACCAAAATCTCCGATCTGCTCTCGACGCTTCGCTTGAACAGACCCAGAC 187  
Db 21 LysLeuCysAspGlnIleSerAspAlaIleLeuAspAlaCysLeuGluGlnAspProAsp 40  
Qy 188 AGCAAGGTGCTCGGAAACATGCACCAAGACCAACTTGGTCATGCTCTCGGAGAGATC 247  
Db 41 SerLysValAlaCysGluThrCysSerLysThrAsnMetValMetIlePheGlyIle 60  
Qy 248 ACCACCAAGGCCAAGCTTGACTACGAGAAGATCGTGGCTGACACCTGACGAGAACATCCGC 307  
Db 61 ThrThrLysAlaAsnValAspTyrGluLysIleValArgAspThrCysArgAlaIleGly 80  
Qy 308 TTCGTCTCAAAACGATGTGGGACTTGAATGCTGACAACTGCAAGGTCTTGTAAACATTGAG 367  
Db 81 PheValSerAspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGlu 100  
Qy 368 CAGCAGACCTTGATATTGCCAGGGTGTGACGCCACCTTACCAAGACCCGAGAA 427  
Db 101 GlnGlnSerProAspIleAlaGlnGlyValHisGlyHisPheThrLysArgProGluGlu 120

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QY 428 ATCGGTGCTGGACAGCGGTACATGTTGGCTATGCTCCAGCAAGAAACCCAGAAATG 487
DB 121 IIEGLYALAGLYASPGINGLYHISMETPHEGLYTYRALATHRAEPGLUThrProGluLeu 140
QY 488 ATGCCATTGAGTCATGTTCTTCAACTAACTCGGTGCTCGTCTCACCGAGTTGCGAAG 547
DB 141 MetProLeuSerHisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLys 160
QY 548 AACGGAACCTGCCCATGTTGAGGCTGTATGGGAAACCAAGTGAATGCTGTGAGTATTAC 607
DB 161 AsnGlyThrCysProTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrArg 180
QY 608 ATGCAACAGCTGCCATGTTCCAGTTCAGTTCGTGTCACACATGTCCTTATCTCCACCAACAT 667
DB 181 AsnAspGlyGlyAlaMetValProIleArgValHisThrValLeuIleSerThrGlnHis 200
QY 668 GATGAGACTGTGACCAACAGCAAAATTCGACGTGACCTCAAGGAGCATGTGATCAAGCCG 727
DB 201 AspGluThrValThrAsnAspGluIleAlaAspLeuLysGluHisValIleLysPro 220
QY 728 GTGATCCCGAGAGTACCTTGTATGAGAGACCATTTTCCACTTGAACCCCTCTGCCCT 787
DB 221 ValValProGluGlnTrpLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArg 240
QY 788 TTTGTCAATGAGGCTCCTCAGGTGATGCTGTCTCACCAGCGCGCAAGATCATCATCAT 847
DB 241 PheValIleGlyGlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleIleAsp 260
QY 848 ACTTACGAGGAGTGGGTGCTCATGTTGTTGTTGTTCTTCTCGGAGGATCCCAACCAAG 907
DB 261 ThrTyrGlyGlyTrpGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLys 280
QY 908 GTTGATAGGAGTGGTCTTACATTTGTGACACAGGCTGCTTAAGAGCATTTGTGCAAGTGA 967
DB 281 ValAspArgSerGlyAlaTyrIleValArgGlnAlaAlaLysSerValValIleAsnGly 300
QY 968 CTAGCCAGAGTGTGATTTCAAGGCGGTATGATCTCCATCAACTTGATCTCAAGAGGGGT 1147
DB 301 LeuAlaArgArgCysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSer 320
QY 1028 GTCCTTGTGACACTATGCGACCGGAGATCCATGATGAAGAGATTTCTCAACATTTG 1087
DB 321 ValPheValAspThrTyrGlyThrGlyLysIleProAspLysGluIleLeuLysIleVal 340
QY 1088 AAGGAGAACTTGTGATTTCAAGGCGGTATGATCTCCATCAACTTGATCTCAAGAGGGGT 1147
DB 341 LysGluAsnPheAspPheArgProGlyMetIleThrIleAsnLeuAspLeuLysArgGly 360
QY 1148 GGAATAACAGGTTCTTGAAGACTGCTGCATATGGACACTTCCGAGAGAGACCCCTGAC 1207
DB 361 Gly---AsnArgPheIleLysThrAlaAlaTyrGlyHisPheGlyArgAspAspProAsp 379
QY 1208 TTCACATGGGAAGTGTGTCAGGCCCTCAAGTGGGGAAG 1246
DB 380 PheThrTrpGluValLysProLeuLysTrpAspLys 392

RESULT 13
Q8GTL5 PRELIMINARY; PRT; 429 AA.
AC Q8GTL5;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE S-adenosylmethionine synthase.
GN Name=SAMS;
OS Carica papaya (Papaya).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroside II; Brassicales; Caricaceae; Carica.
OX NCBI_TaxID=3649;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ripening fruit mesocarp;
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RA Kaszinda J., Chong J.Y., Othman R., Ali Z.M., Lazan H.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Catalyzes the formation of S-adenosylmethionine from
CC methionine and ATP (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + L-methionine -> phosphate +
CC diphosphate + S-adenosyl-L-methionine.
CC -!- COFACTOR: Binds 2 divalent ions, such as magnesium or cobalt, and
CC 1 potassium ion per subunit (By similarity).
CC -!- PATHWAY: Activated methyl cycle.
CC -!- SIMILARITY: Belongs to the AdoMet synthetase family.
DR EMBL: AF531479; AAC07179.1; -.
DR HSP: P13444; IQM4.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0000287; F:magnesium ion binding; IEA.
DR GO: GO:0004478; F:methionine adenosyltransferase activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0006730; P:one-carbon compound metabolism; IEA.
DR InterPro: IPR002133; S-AdoMet_synth.
DR Pfam: PF02773; S-AdoMet_synth_C; 1.
DR Pfam: PF00438; S-AdoMet_synth_M; 1.
DR PIRSF: PIRSF000497; MAT; 1.
DR TIGSFAM: TIGSF01034; metK; 1.
DR PROSITE: PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE: PS00377; ADOMET_SYNTHETASE_2; 1.
KW ATP-binding; Magnesium; Metal-binding; One-carbon metabolism;
KW Potassium; Transferase.
SQ SEQUENCE 429 AA; 47085 MW; 905E68EA23F37112 CRC64;

Alignment Scores:
Pred. No.: 1.62e-144 Length: 429
Score: 1972.50 Matches: 381
Percent Similarity: 89.04% Conservative: 17
Best Local Similarity: 85.23% Mismatches: 26
Query Match: 71.78% Indels: 23
DB: 2 Gaps: 4

US-10-734-698A-38 (1-1485) x Q8GTL5 (1-429)
QY 80 GAGACATTCCTATTATTTACCTCAGAGTCAGTGAACGAGGACACCCCTGACAGCTCTGCGAC 139
DB 2 GluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCysAsp 21
QY 140 CAATCTCCGATGCTGCTCTCGACCTTGCCTTGAACAGGACCCAGACAGCAAGGTGCTGCC 199
DB 22 GlnIleSerAspAlaValLeuAspAlaCysLeuAlaGlnAspProAspSerLysValAla 41
QY 200 TCGGAAACATGCAACCAAGCCAACTTGTGTCATGCTTCGGAGAGATCACCAAGGCC 259
DB 42 CysGluThrCysThrLysThrAsnMetValMetValPheGlyGluIleThrThrLysAla 61
QY 260 AACGTTGACTACGAGAAGATCGTGGTCACACCTCGAGAACATCGCTTCGCTCTCAAC 319
DB 62 AspValAspTyrGluLysIleValArgAspThrCysArgSerIleGlyPheValSerAsp 81
QY 320 GATGTGGACTTGATGCTGACAACTGCAAGGTCTTTGTAACATTTGAGCAGCAGAGCCCT 379
DB 82 AspValGlyLeuAspAlaAspLysCysLysValLeuValAsnIleGluGlnSerPro 101
QY 380 GATATTGCCAGGTTGTCAGCGCCACTTACCAGGAGAACCCGAGGAAATCGGCTGGA 439
DB 102 AspIleAlaGlnGlyValHisGlyHisPheThrLysArgProGluGluIleGlyAlaGly 121
QY 440 GACCAAGGTCATGTTTGGTGTATGCCACGAGCAAAACCCCAAGATTGATGCTTGAAT 499
DB 122 AspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluPheMetProLeuSer 141
QY 500 CATGTTCTTGCAACTAAACTCGGTGCTGCTCTCACCGAGGTTTCGCAAGAACGCACTGCG 559
DB 142 HisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThrCys 161
QY 560 CCATGGTTGAGCCCTGATGGGAAACCCCAAGTACTGTGTAGTATTACATGACCAACGGT 619
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Db 162 ArgTrpLeuLysProAspGlyLysThrGlnValThrValGluTyrCysAsnAspAenGly 181  
 QY 620 GCCATGTTCCAGTTCGTGCCACACTGTCTTATCTCCACCAACATGATGAGACTGTG 679  
 Db 182 AlaMetIleProIleArgValHisThrValLeuIleSerThrGlnHisAspGluThrVal 201  
 QY 680 ACCAAGCAGCAAAATCCAGCTGACCTCAGGACATGTGATCAAGCGGTGATCCCGGAG 739  
 Db 202 ThrAsnAspGluIleAlaArgAspLeuLysGluHisAlaIleLysProValIleProGlu 221  
 QY 740 AAGTACCTTGATGAGAAAGACCATTTCCACTTCAACCCCTCTGCCGCTTTGTGCTTGA 799  
 Db 222 LysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheValIleGly 241  
 QY 800 GGTCTCAGCGTATGCTGTCTCACCGGCCGCAAGATCATCATCATCTTACGAGAGA 859  
 Db 242 GlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleIleAspThrTyrGlyGly 261  
 QY 860 TGGGGTCTCATGTTGGTGTGCTTTCTCCGGGAAGATCCCAACCAAGTTGATGAGGT 919  
 Db 262 TrpGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSer 281  
 QY 920 GGTCTTACATTCGTGAGACAGGCTGTAGAGCATTTGTGCAAGTGTGCAAGCAAG 979  
 Db 282 GlyAlaTyrIleValArgGlnAlaAlaLysSerIleValAlaSerGlyLeuAlaArg 301  
 QY 980 TGCAATGTGCAAGTCTTATGCAATTTGCTGCTGCCGAGCTTTGTCTGTTGTGAC 1039  
 Db 302 CysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAsp 321  
 QY 1040 ACCTATGGACCCGGGAAGATCCATGATATAGGAGATTCTCAACATTTGAAAGGAACTTT 1099  
 Db 322 ThrTyrGlyThrGlyLysIleProAspArgGluIleLeuLysIleValLysGluAsnPhe 341  
 QY 1100 GATTTCAGGCCGGTATGATCTCCATCACTTGATCTCAAGGGGTGGATTAACAGG 1159  
 Db 342 AspPheArgProGlyMetSerIleAsnLeuAspLeuLysArgGlyGlyAsnGlyArg 361  
 QY 1160 TTCTTAAGACTGCTGCATATGACACTTCGGCAGAGAGACCTGACTTCACTGCGGAA 1219  
 Db 362 PheLeuLysThrAlaAlaTyrGlyHisPheGlyArgAspAspAlaAspPheThrTrpGlu 381  
 QY 1220 GTGGTCAAGCCCTCAAGTGGGAG 1243  
 Db 382 ValValLysProLeuLysTrpGlu 389

## RESULT 15

Q9FUZ1 PRELIMINARY; PRT; 393 AA.  
 AC Q9FUZ1; (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE S-adenosylmethionine synthetase.  
 OS Brassica juncea (leaf mustard) (Indian mustard).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Brassicales; Brassicaceae; Brassica.  
 OX NCBI\_TaxID=3707;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Liu J.-Z., Pua E.-C.;  
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Catalyzes the formation of S-adenosylmethionine from  
 CC methionine and ATP (By similarity).  
 CC -!- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +  
 CC diphosphate + S-adenosyl-L-methionine.  
 CC -!- COFACTOR: Binds 2 divalent ions, such as magnesium or cobalt, and  
 CC 1 potassium ion per subunit (By similarity).  
 CC -!- PATHWAY: Activated methyl cycle.  
 CC -!- SIMILARITY: Belongs to the AdoMet synthetase family.  
 CC EMBL; AF271220; AAG17666.1; -.  
 DR HSP; P13444; 1QM4.

DR GO: 0005524; F:ATP binding; IEA.  
 DR GO: 0000287; F:magnesium ion binding; IEA.  
 DR GO: 0004478; F:methionine adenosyltransferase activity; IEA.  
 DR GO: 0016740; F:transferase activity; IEA.  
 DR GO: 0006730; P:one-carbon compound metabolism; IEA.  
 DR InterPro: IPR002133; S-AdoMet synt.  
 DR Pfam: PF02773; S-AdoMet synt\_C; 1.  
 DR Pfam: PF02772; S-AdoMet synt\_M; 1.  
 DR Pfam: PF00438; S-AdoMet synt\_N; 1.  
 DR PIRSF: PIRSF000497; MAT; 1.  
 DR TIGRFAMs: TIGR01034; metK; 1.  
 DR PROSITE: PS00376; ADOMET\_SYNTHETASE\_1; 1.  
 DR PROSITE: PS00377; ADOMET\_SYNTHETASE\_2; 1.  
 KW ATP-binding; Magnesium; Metal-binding; One-carbon metabolism;  
 KW Potassium; Transferase.  
 SQ SEQUENCE 393 AA; 42879 MW; 65BDAC0A52576122 CRC64;

## Alignment Scores:

Pred. No.: 1.48e-143 Length: 393  
 Score: 1960.00 Matches: 367  
 Percent Similarity: 97.94% Conservative: 14  
 Best Local Similarity: 94.34% Mismatches: 8  
 Query Match: 71.32% Indels: 0  
 DB: 2 Gaps: 0

US-10-734-698A-38 (1-1485) x Q9FUZ1 (1-393)

QY 80 GAGCATTTCCCTATTATTTACCTCAGAGTCAGTCAACGAGGAGACACCTTGACAGAGCTCTGGAC 139  
 Db 2 GluSerPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCysAsp 21  
 QY 140 CAAATCTCCGATGCTGCTCGACGCTTGCCTTGAACAGGACCCACAGACAGCAAGGTGCG 199  
 Db 22 GlnIleSerAspAlaIleLeuAspAlaCysLeuGluGlnAspProGluSerLysValAla 41  
 QY 200 TCGGAAACATGCACCAAGACCAACTTGTGTCATGTCTTCGAGAGATCACCACCAAGGCC 259  
 Db 42 CysGluThrCysThrLysThrAsnMetValMetValPheGlyGluIleThrThrLysAla 61  
 QY 260 AACGTTGACTACGAGAGATCGTGGTCACACCTCGCAGGACATCGCTCTCTCAAC 319  
 Db 62 AsnValAspTyrGluLysIleValArgGluThrCysArgGluIleGlyPheIleSerAsp 81  
 QY 320 GATGTGGGACTTGATGTCACAACTGCAAGGTCCTTTGAAACATTGAGCAGCAGAGCCCT 379  
 Db 82 AspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGlnSerPro 101  
 QY 380 GATATTGCCAGGTGTGCACGGCCACTTACCAGGAGCCGAGGAAATCGGTCTGGA 439  
 Db 102 AspIleAlaGlnGlyValHisGlyHisLeuThrLysLysProGluGluIleGlyAlaGly 121  
 QY 440 GACCAAGGTTCATGTTGGCTATGCCACGACGAGAACCCCAAGATTGATGCCATTGAT 499  
 Db 122 AspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuSer 141  
 QY 500 CATGTTCTTGCAACTAAACTCGGTGCTGCTCTCACCGAGGTTCGCAAGAACCGAACCTGC 559  
 Db 142 HisValLeuAlaThrLysLeuGlyAlaLysLeuThrGluValArgLysAsnGlyThrCys 161  
 QY 560 CCATGGTTGAGGCTGTATGGGAAACCAACCAAGTGAAGTGTGTGATTTACATGACACACGGT 619  
 Db 162 AlaTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrPheAsnGluAsnGly 181  
 QY 620 GCCATGTTCCAGTTCGTGCTCCACACTGTCTTATCTCCACCAACATGATGAGACTGTG 679  
 Db 182 AlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGluThrVal 201  
 QY 680 ACCAAGCAGCAAAATTCGAGCTGACCTCAAGGAGCATGTGATCAAGCGGTGATCCCGGAG 739  
 Db 202 ThrAsnAspGluIleAlaAspLeuLysIleValIleLysProValIleProGlu 221  
 QY -740 AAGTACCTTGATGAGAGACCATTTTCCACTTGAACCCCTCTGCGCGCTTTGTGCTTGA 799

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Db      222 LysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheValIleGly 241
QY      800 GGTCTCTACGGTGATGCTGCTACCGGCCCAAGATCATCATCTTACGGAGGA 859
        |||
Db      242 GlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyrGlyGly 261
QY      860 TGGGGTGCTCATGGTGCTGCTTCTCCGGGAAGGATCCCAACAAGTTGATAGGAGT 919
        |||
Db      262 TrpGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSer 281
QY      920 GGTGCTTACATTGTGAGCAGGCTGCTAAGAGCATTGTGGCAAGTGGACTAGCCAGAAGG 979
        |||
Db      282 GlyAlaTyrIleValArgGlnAlaLysSerIleValAlaSerGlyLeuAlaArgArg 301
QY      980 TGCATTGTGCAAGTGCTTATGCCATTGGTGCCCGAGCCTTTGCTCTGCTTTGTTGAC 1039
        |||
Db      302 CysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAsp 321
QY      1040 ACCTATGGCACCGGAAGATCCATGATAAGGAGATTCTCAACATTGTGAAGGAGACTTT 1099
        |||
Db      322 SerTyrGlyThrGlyLysIleProAspLysGluIleLeuGluIleValLysGluSerPhe 341
QY      1100 GATTTCAAGCCCGGTATGATCTCCATCAACCTTGATCTCAAGAGGGGTGGGAATAACAGG 1159
        |||
Db      342 AspPheArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyGlyAsnGlyArg 361
QY      1160 TTCCTGAAGACTGCTGCATATGGACACTTCGGCAGAGAGGACCCCTGACTTCAATGGGAA 1219
        |||
Db      362 PheLeuLysThrAlaAlaTyrGlyHisPheGlyArgAspAlaAspPheThrTrpGlu 381
QY      1220 GTGGTCAAGCCCTCAAGTGGGAGAAG 1246
        |||
Db      382 ValValLysProLeuLysSerAsnLys 390
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Job time : 298.5 secs